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Limits		Index	History	Clipboard			
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☐ 1: CAA70330 **dioxygenase** BLink, PubMed, Related Sequences, Nucleotide, Taxonomy
[Marah macrocarpus]

LOCUS CAA70330 322 aa PLN 01-MAY-1997
 DEFINITION dioxygenase [Marah macrocarpus].
 ACCESSION CAA70330
 PID g1666096
 VERSION CAA70330.1 GI:1666096
 DBSOURCE embl locus MMY09113, accession Y09113.1
 KEYWORDS .
 SOURCE Marah macrocarpus.
 ORGANISM Marah macrocarpus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 Rosidae; Cucurbitales; Cucurbitaceae; Marah.

REFERENCE 1 (residues 1 to 322)
 AUTHORS MacMillan, J., Ward, D.A., Phillips, A.L., Sanchez-Beltran, M.J.,
 Gaskin, P., Lange, T. and Hedden, P.
 TITLE Gibberellin biosynthesis from gibberellin A12-aldehyde in endosperm
 and embryos of Marah macrocarpus
 JOURNAL Plant Physiol. 113 (4), 1369-1377 (1997)
 MEDLINE 97267151

REFERENCE 2 (residues 1 to 322)
 AUTHORS Hedden, P.
 TITLE Direct Submission
 JOURNAL Submitted (31-OCT-1996) P. Hedden, University of Bristol,
 Department of Agricultural Sciences, IACR-Long Ashton Research
 Station, Long Ashton, Bristol, BS18 9AF, UK

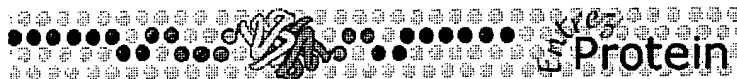
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 121 klrsalndyi wavrmacei velmaeglki qqrnalskll mgeesdsivr vnhyppcpee
 181 lqalegtmni gfgehtdpqi isvlrsnnts glqislpdan wisvppdqt ffinvgdslq
 241 vmtngrfksv khrltnslk srismiyyfgg pplsekiapl pslmkgeesl ykeftwfeyk
 301 rsaynsrlad nrlvhferia as

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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	
Search	Protein	for					Go	Clear
Limits		Index	History		Clipboard			
Display	Default View	as	HTML	Save	Add to Clipboard			

☐ 1: [AAD04293](#) **copalyl diphosphate synthase 2; CPS2 [Cucurbita maxima]** BLink, PubMed, Related Sequences, Nucleotide, Taxonomy

LOCUS AAD04293 827 aa PLN 13-JAN-1999
 DEFINITION copalyl diphosphate synthase 2; CPS2 [Cucurbita maxima].
 ACCESSION AAD04293
 PID g4151195
 VERSION AAD04293.1 GI:4151195
 DBSOURCE locus AF049906 accession [AF049906.1](#)
 KEYWORDS .
 SOURCE winter squash.
 ORGANISM *Cucurbita maxima*
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 Cucurbitales; Cucurbitaceae; Cucurbita.

REFERENCE 1 (residues 1 to 827)
 AUTHORS Smith,M.W., Yamaguchi,S., Ait-Ali,T. and Kamiya,Y.
 TITLE The first step of gibberellin biosynthesis in pumpkin is catalyzed by at least two copalyl diphosphate synthases encoded by differentially regulated genes
 JOURNAL Plant Physiol. 118 (4), 1411-1419 (1998)
 MEDLINE 99063778

REFERENCE 2 (residues 1 to 827)
 AUTHORS Smith,M.W., Yamaguchi,S., Ait-Ali,T. and Kamiya,Y.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-1998) Plant Hormone Function Lab, Frontier Research Program, Institute of Physical and Chemical Research (RIKEN), Hirosawa 2-1, Wako-shi 351-0198, Japan

COMMENT Method: conceptual translation supplied by author.

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 301 pastafalmh tnhpncfkyl easvhrfngg vpvvypvdlf ehiwavdrfq rlgisrffhp
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☐ 1: T02959 **kaurene synthase A - maize** BLink, PubMed, Related Sequences, Taxonomy

LOCUS T02959 823 aa PLN 29-OCT-1999
 DEFINITION kaurene synthase A - maize.
 ACCESSION T02959
 PID g7489781
 VERSION T02959 GI:7489781
 DBSOURCE pir: locus T02959;
 summary: #length 823 #molecular-weight 95122 #checksum 392;
 genetic: #gene AN1;
 PIR dates: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-Oct-1999.

KEYWORDS

SOURCE

Zea mays.

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

REFERENCE

AUTHORS

Bensen, R.J., Johal, G.S., Crane, V.C., Tossberg, J.T., Schnable, P.S., Meeley, R.B. and Briggs, S.P.

TITLE

Cloning and characterization of the maize An1 gene

JOURNAL

Plant Cell 7 (1), 75-84 (1995)

MEDLINE

95210929

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source

Location/Qualifiers

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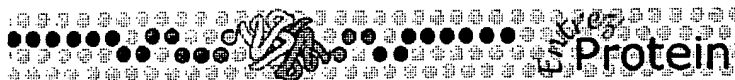
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661 hllslawte wmlqkankee nkyhkcsgie pqymvhdrqt ylllvqviei cagrigaavs
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Limits		Index	History	Clipboard			
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: AAB87091 **copalyl pyrophosphate synthase [Stevia rebaudiana]** BLink, PubMed, Related Sequences, Nucleotide, Taxonomy

LOCUS AAB87091 787 aa PLN 22-MAR-2000
 DEFINITION copalyl pyrophosphate synthase [Stevia rebaudiana].
 ACCESSION AAB87091
 PID g2642661
 VERSION AAB87091.1 GI:2642661
 DBSOURCE locus AF034545 accession AF034545.1
 KEYWORDS .
 SOURCE Stevia rebaudiana.
 ORGANISM Stevia rebaudiana
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
 II; Asterales; Asteraceae; Asteroideae; Heliantheae; Stevia.

REFERENCE 1 (residues 1 to 787)
 AUTHORS Richman,A.S., Gijzen,M., Starratt,A.N., Yang,Z. and Brandle,J.E.
 TITLE Diterpene synthesis in Stevia rebaudiana: recruitment and
 up-regulation of key enzymes from the gibberellin biosynthetic
 pathway
 JOURNAL Plant J. 19 (4), 411-421 (1999)
 MEDLINE 99435880
 PUBMED 10504563

REFERENCE 2 (residues 1 to 787)
 AUTHORS Richman,A.S., Gijzen,M. and Brandle,J.E.
 TITLE Direct Submission
 JOURNAL Submitted (13-NOV-1997) Research Branch, Agriculture and Agri-Food
 Canada, 1391 Sandford St., London, ON N5V 4T3, Canada

COMMENT Method: conceptual translation supplied by author.

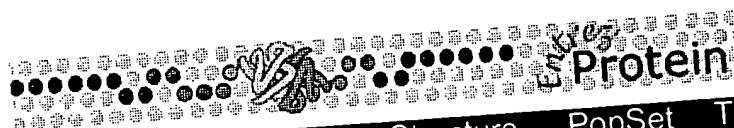
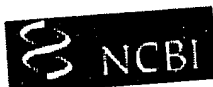
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 CDS 1..787
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 121 qdvdgsgspq fpsslewian nqlsdgswgd hllfsahdri intlacvial tswnvhpskc
 181 ekglfnlren ickledenae hmpigfevtf pslidiakkl nievpdtpa lkeiyarrdi
 241 kltkipmevl hkvpttllhs legmpdlewe klklqckdg sflfsssta falmqtkdek
 301 clqyltnivt kfnggvpnvy pvdlfehiww vdrqlrgia ryfkseikdc veyinkywtk
 361 ngicwarntv vqdiddtamg frvlrahgyd vtpdvfrqfe kdqkfvcfag qstqavtgmf
 421 nvyrasqmlf pgeriledak kfsynylkek qstnellkw iiakdlpgev gyal dipwya
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541 qwyvdigiek fesdniksvl vsyylaaasi feperskeri awaktilvd kitsifdssq
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661 qawemwltkl qdgvdvtael mvqminmtag rwvskellth pqyqrlstvt nsvchditkl
721 hnfkensttv dskvqelvql vfsdtpddld qdmkqtfltv mktfyykawc dpntindhis
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PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

Search Protein ☐ for ☐ Limits Index History Clipboard

Display Default View ☐ as HTML ☐ Save Add to Clipboard

BLINK, PubMed, Related Sequences, Nucleotide, Taxonomy

☐ 1: AAB39482 **ent-kaurene
synthase B
[Cucurbita
maxima]**

PLN

30-DEC-1996

LOCUS AAB39482 789 aa
 DEFINITION ent-kaurene synthase B.
 ACCESSION AAB39482
 PID g1431870
 VERSION AAB39482.1 GI:1431870
 DBSOURCE locus CMU43904 accession U43904.1

KEYWORDS winter squash.
 SOURCE Cucurbita maxima

ORGANISM Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 Cucurbitales; Cucurbitaceae; Cucurbita.

REFERENCE 1 (residues 1 to 789)
 AUTHORS Yamaguchi, S., Saito, T., Abe, H., Yamane, H., Murofushi, N. and
 Kamiya, Y.

TITLE Molecular cloning and characterization of a cDNA encoding the
 gibberellin biosynthetic enzyme ent-kaurene synthase B from pumpkin
 (Cucurbita maxima L.)
 JOURNAL Plant J. 10 (2), 203-213 (1996)

MEDLINE 96367664
 REFERENCE 2 (residues 1 to 789)
 AUTHORS Yamaguchi, S., Saito, T., Abe, H., Yamane, H., Murofushi, N. and
 Kamiya, Y.

TITLE Direct Submission
 JOURNAL Submitted (25-DEC-1995) Shinjiro Yamaguchi, The Institute of
 Physical and Chemical Research, Hirosawa2-1, Wako-shi, Saitama
 351-01, Japan

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181 nvdalvrkke lelrsrsns eggkaylayv segigklqdw dmvmqyqrkn gslfnspstt
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661 gsceyqklyk lmstagrln dirsydreck egklnilslw midgggnvtnk eeaieaikgd
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781 mldallnk
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Limits Index History Clipboard							
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☐ 1: AAB58822 **ent-kaurene synthase A** [Pisum sativum] BLink, PubMed, Related Sequences, Nucleotide, Taxonomy

LOCUS AAB58822 801 aa PLN 05-JUN-1997
 DEFINITION ent-kaurene synthase A [Pisum sativum].
 ACCESSION AAB58822
 PID g2160544
 VERSION AAB58822.1 GI:2160544
 DBSOURCE locus PSU63652 accession U63652.1
 KEYWORDS .
 SOURCE pea.
 ORGANISM Pisum sativum
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 Fabales; Fabaceae; Papilionoideae; Pisum.

REFERENCE 1 (residues 1 to 801)
 AUTHORS Ait-Ali,T., Swain,S.M., Reid,J.B., Sun,T.-p. and Kamiya,Y.
 TITLE The LS locus of pea encodes the gibberellin biosynthesis enzyme
 ent-kaurene synthase A
 JOURNAL Plant J. 11 (3), 443-454 (1997)
 MEDLINE 97260958

REFERENCE 2 (residues 1 to 801)
 AUTHORS Ait-Ali,T., Swain,S.M., Reid,J.B., Sun,T.-p. and Kamiya,Y.
 TITLE Direct Submission
 JOURNAL Submitted (12-JUL-1996) Plant Hormone Function, RIKEN Institute,
 Hirosawa 2-1, Wako-shi, Saitama 351-01, Japan

COMMENT Method: conceptual translation.

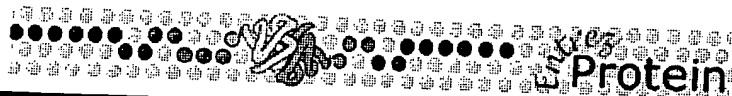
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 Protein 1..801
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 /product="ent-kaurene synthase A"
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☐ 1: CAA03884 GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phosphate synthase [Arabidopsis thaliana] BLink, Related Sequences, Nucleotide,

LOCUS CAA03884 543 aa PLN 02-OCT-1997
 DEFINITION GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phosphate synthase [Arabidopsis thaliana].
 ACCESSION CAA03884
 PID g2462925
 VERSION CAA03884.1 GI:2462925
 DBSOURCE embl locus ATAJ0053, accession AJ000053.1
 KEYWORDS
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllphytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 543)
 AUTHORS Herz, S.W.
 TITLE Direct Submission
 JOURNAL Submitted (31-JUL-1997) Herz S.W., Institut fuer Org. Chemie und Biochemie, TU Muenchen, Lichtenbergstr. 4, 85747 Garching, FRG
 REFERENCE 2 (residues 1 to 543)
 AUTHORS Herz, S.W., Eberhardt, S. and Bacher, A.
 TITLE Biosynthesis of riboflavin in plants. The ribA gene of Arabidopsis thaliana specifies a bifunctional GTP cyclohydrolase II / 3,4-dihydroxy-2butanone-4-phosphate synthase
 JOURNAL Unpublished
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 Protein 1..543
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 CDS 1..543
 /gene="ribA"
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 121 ldlptpgfss ipeaiedirg gklvvvdde drenegdlvm aaqlatpeam afivrhgtgi
 181 vcvsmeddl erhlplmvn qkeneeklst aftvtvdakh gtttgsard rattilslas
 241 rdskpedfmr pghifplkyr eggvlkragh teasvdltrl agldpvgvlc eivddgmsa
 301 rlpklrefaa ennlkvvsia dliryrkrd klverasaar iptmwgpfta ycyrsildgi
 361 ehiamvkgei gdgqdlrvv hsecltgdlf gsarcdgnq lalsmqiea tgrgvlylr
 421 ghegrgiglg hklraynlqd agrdtveane elglpvsre ygigaqiird lgvrtmklmt
 481 nnpakyvglk gyglaiivgrv plslitken kryletkrk mghmyglkfk gdvvekie
 541 ses



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	
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Limits		Index	History	Clipboard				
Display	Default View	as	HTML	Save	Add to Clipboard			

☐ 1: AAC39443 **ent-kaurene synthase**
[Arabidopsis thaliana] BLink, PubMed, Related Sequences, Nucleotide, Taxonomy

LOCUS AAC39443 785 aa PLN 17-APR-1998
 DEFINITION ent-kaurene synthase [Arabidopsis thaliana].
 ACCESSION AAC39443
 PID g3056725
 VERSION AAC39443.1 GI:3056725
 DBSOURCE locus AF034774 accession AF034774.1
 KEYWORDS .
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 785)
 AUTHORS Yamaguchi, S., Sun, T., Kawaide, H. and Kamiya, Y.
 TITLE The GA2 locus of Arabidopsis thaliana encodes ent-kaurene synthase
 of gibberellin biosynthesis
 JOURNAL Plant Physiol. 116 (4), 1271-1278 (1998)
 MEDLINE 98205064
 REFERENCE 2 (residues 1 to 785)
 AUTHORS Yamaguchi, S., Sun, T.-P., Kawaide, H. and Kamiya, Y.
 TITLE Direct Submission
 JOURNAL Submitted (14-NOV-1997) Botany, Duke University, Research Dr.,
 Durham, NC 27708, USA
 COMMENT Method: conceptual translation supplied by author.
 FEATURES Location/Qualifiers
 source 1..785
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /chromosome="1"
 Protein 1..785
 /function="terpene cyclase"
 /product="ent-kaurene synthase"
 CDS 1..785
 /gene="GA2"
 /coded_by="AF034774.1:68..2425"

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 61 vamvpsspssq naplfpqcvk wlldnqheda swgldnhdhq slkkdvlst lasilalkkw
 121 gigerqinkg lqfielnsal vtdetiqtpt gfdiifpgmi kyardlnlti plgsevvddm
 181 irkrldldkc dsekfskgre aylayvlegt rnlkdwdliv kyqrkngslf dspattaaaf
 241 tqfgndgclr ylcsllqkfe aavpsvypfd qyarlsiivt leslgidrdf kteiksilde
 301 tyrywlrge eicldlatca lafrlllahg ydvsydpkpk faeesgfsdt legyvknfts
 361 vlelfkaaqs yphesalkkq ccwtkqylem elsswvktsv rdkylkkeve dalafpsyas
 421 lersdhrarki lngsaventv vtktysrlhn ictsdilkla vddfnfcqsi hreemerldr
 481 wivenrlqel kfarqklayc yfsgaatlfs pelsdarisw akggvlttvv ddfdvvggsk
 541 eelenlihlv ekwdlngvpe yssehveiif svlrtdilet gdkaftyqgr nvthhivkiw
 601 ldllksmlre aewssdkstp sledymenay isfalgpivl patyligppl pektvdshqy
 661 nqglyklvstm grllndiqgf kresaegkln avslhmkher dnrskeviie smkglaerkr
 721 eelhlklvlee kgsvvpreck eafikmskvl nlfyrkddgf tsndlmslvk sviyepvslq

781 keslt

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[NCBI](#) | [NLM](#) | [NIH](#)



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search	Protein	for		Go	Clear		
Limits		Index		History		Clipboard	
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: AAC31213 **ethylene receptor homolog** BLink, Related Sequences, Nucleotide, Taxonomy
[*Nicotiana tabacum*]

LOCUS AAC31213 762 aa PLN 16-AUG-1999
 DEFINITION ethylene receptor homolog [*Nicotiana tabacum*].
 ACCESSION AAC31213
 PID g5733831
 VERSION AAC31213.3 GI:5733831
 DBSOURCE locus AF026267 accession AF026267.3
 KEYWORDS .
 SOURCE common tobacco.
 ORGANISM *Nicotiana tabacum*
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
 I; Solanales; Solanaceae; *Nicotiana*.
 REFERENCE 1 (residues 1 to 762)
 AUTHORS Zhang, J.-S. and Chen, S.-Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-AUG-1999) 803 Lab, Institute of Genetics, Academia
 Sinica, Beijing 100101, PRC
 REMARK Sequence update by submitter
 COMMENT On Aug 16, 1999 this sequence version replaced gi:4982466.
 Method: conceptual translation.
 FEATURES
 source 1..762
 /organism="Nicotiana tabacum"
 /db_xref="taxon:4097"
 Protein 1..762
 /product="ethylene receptor homolog"
 CDS 1..762
 /gene="NTHK1"
 /coded_by="AF026267.3:247..2535"

ORIGIN

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1 mlrtlalall isafvlslsa adngfprcnc ddegfwsier ilecqrisd1 fiaiaysip
61 iellyfvscs nfpfkwlflq fiafivlcmg thllnfwtyy gqhpqqlmla ltifkvltal
121 vsfataitli tlfpmllkik vrefmlkkkt wdlgrevgli kqqkeagwhv rmltqeirks
181 ldrhtilytt lvelaktldl hncaiwpne nktemnlihe lkgrsfssmy nlpiptsdpd
241 vreikesdgv klldayspla aassggssep gavaaairmpm lkvsnfkggt pelvpeyai
301 lvlvlpgeqg rswsnqeiei vrvvadqvav alshaavlee sqhmretlee qnralqqakq
361 dalrasqarn afqmvmsghl rrpmsilgl lsllqddnmg ieqrllvdam aktssvvstl
421 indvmdtstk dnsrfplemr hfqlhsmike aacalaklca hrgynisiev dkslpnyvmg
481 derrvfqvil hmvgnllkdp nggcldtfrvl pesarregid gawktrrshs slenvyirfe
541 vgssnnhsqp egitstlphc cetrssreve erlsfsvcrk lvqlmqgdiw vvpnpegfdq
601 smtvilgflq rpsiavgipe ygessdhshp hsllqgvnvl ladyddvnra vtrkllek1g
661 ctvsavssgh dclgalgpav ssfqivlldl hlpdldgfev tmrيرهfrsr nwplivgfas
721 adedvsgrcl qigmgngiirk pvllpgiade lqrvllqasi it

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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search Protein		for					Go Clear
Limits		Index	History	Clipboard			
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: [AAC13635](#) **F6N23.3 gene product** BLink, Related Sequences, Nucleotide, Taxonomy
[*Arabidopsis thaliana*]

LOCUS AAC13635 213 aa PLN 12-NOV-1999
 DEFINITION F6N23.3 gene product [*Arabidopsis thaliana*].
 ACCESSION AAC13635
 PID g3047124
 VERSION AAC13635.1 GI:3047124
 DBSOURCE locus F6N23 accession [AF058919.2](#)
 KEYWORDS .
 SOURCE thale cress.
 ORGANISM *Arabidopsis thaliana*
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 213)
 AUTHORS Geisel,C.
 TITLE The sequence of *A. thaliana* F6N23
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 213)
 AUTHORS Washington University Genome Sequencing Center.
 TITLE The *A. thaliana* Genome Sequencing Project
 JOURNAL Unpublished
 REFERENCE 3 (residues 1 to 213)
 AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (10-APR-1998) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 REFERENCE 4 (residues 1 to 213)
 AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (12-NOV-1999) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT Method: conceptual translation.
 FEATURES
 source Location/Qualifiers
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 /organism="Arabidopsis thaliana"
 /cultivar="Columbia"
 /db_xref="taxon:3702"
 /chromosome="IV"
 /map="unknown"
 /clone="F6N23"
 Protein 1..213
 CDS 1..213
 /gene="F6N23.3"
 /coded_by="join(AF058919.2:16976..17111,
 AF058919.2:17262..17415,AF058919.2:17785..17889,
 AF058919.2:18316..18417,AF058919.2:18618..18666,
 AF058919.2:19056..19151)"
 ORIGIN
 1 meiysnhcdt tvyasqalaa asktvetmki vhnfhcyfll vgdinipiiy dvnrlrdggn
 61 fatrsvdarq kgktiftlfa sfqvsyipe ifhyesldyr nqvateisvp fpidirfcep
 121 nrstkqnksp prcvvafasd lifatislnp hrregmsvaa lsldhsmwfh rpvraddwll
 181 fvivspstate srgfatgkmf nrkgvvrcci eee



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search	Protein	for					Go
Limits		Index	History	Clipboard			
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: [AAD31397](#) **ethylene receptor homolog [Lycopersicon esculentum]** BLink, PubMed, Related Sequences, Nucleotide, Taxonomy

LOCUS AF118844_1 767 aa PLN 20-MAY-1999
 DEFINITION ethylene receptor homolog [Lycopersicon esculentum].
 ACCESSION AAD31397
 PID g4877653
 VERSION AAD31397.1 GI:4877653
 DBSOURCE locus AF118844 accession [AF118844.1](#)
 KEYWORDS .
 SOURCE tomato.
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
 REFERENCE 1 (residues 1 to 767)
 AUTHORS Tieman, D.M. and Klee, H.J.
 TITLE Differential expression of two novel members of the tomato ethylene-receptor family
 JOURNAL Plant Physiol. 120 (1), 165-172 (1999)
 MEDLINE 99252262
 REFERENCE 2 (residues 1 to 767)
 AUTHORS Tieman, D.M. and Klee, H.J.
 TITLE Direct Submission
 JOURNAL Submitted (08-JAN-1999) Horticultural Sciences, University of Florida, P.O. Box 110690, Gainesville, FL 32611, USA
 COMMENT Method: conceptual translation supplied by author.
 FEATURES
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 Location/Qualifiers
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 /organism="Lycopersicon esculentum"
 /strain="Rutgers"
 /db_xref="taxon:4081"
 Protein
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 /product="ethylene receptor homolog"
 /name="similar to Arabidopsis thaliana ETR1"
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 /gene="ETR5"
 /coded_by="AF118844.1:681..2984"

ORIGIN

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121  alvscatait  lltliplllk  ikvrelflaq  nvleldqevg  mmkkqteasm  hvrmltheir
181  ksldkhtily  ttlvelsktl  klqncavwmp  nesrsqmnlt  helpssaae  shrslsindp
241  dvleitknkg  vrilrqdsvl  aasssggsge  pcavaairmp  llrasdfkkg  tpelvdtrya
301  ilvlvlssvd  ervwsydeme  ivevvadqva  valshatvle  esqtmrekle  mnrnvlqqaq
361  enamkasqar  tsfqkvmnng  mrrpmhsilg  llsifqdeka  ssdqrmiavt  mvktstvlst
421  lindameisa  kddgrfpvem  kpfqlhllvr  easclvklc  vykgfgfst  vptslpnqvm
481  gdekrtfqvl  lhmvgllnv  sigkgsivfr  vvletgaetg  ndkvwgtrrp  sttdeyvtik
541  feievslegs  qsdssistih  fgrrhnske  vteglsfmnc  kklvqmmqgn  iwmssnaqgh
601  aqgmtlilrf  qkqssfrkrm  feyrnpleqp  isstmfrglh  vlltddddvn  rlvtrkllek

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661 lgcqvtavst gfcclsalgp slttfqvlil dlqmpemdgy evalrvrkfr srswpliial
721 tasseeqvwe kclqvgmngl irkpvlqgl adelqrllqr ggggdgl

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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search	Protein	for					Go
Limits		Index	History	Clipboard			
Display	Default View	as	HTML	Save	Add to Clipboard		

1: AAD26899 ethylene receptor homolog BLink, Related Sequences, Nucleotide, Taxonomy [Phalaenopsis sp. 'True Lady']

LOCUS AAD26899 633 aa PLN 17-JUN-1999
 DEFINITION ethylene receptor homolog [Phalaenopsis sp. 'True Lady'].
 ACCESSION AAD26899
 PID g4650821
 VERSION AAD26899.1 GI:4650821
 DBSOURCE locus AF055894 accession AF055894.1
 KEYWORDS
 SOURCE Phalaenopsis sp. 'True Lady'.
 ORGANISM Phalaenopsis sp. 'True Lady'
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Phalaenopsis.
 REFERENCE 1 (residues 1 to 633)
 AUTHORS Do, Y.Y., Chen, Y.C. and Huang, P.L.
 TITLE Molecular Analysis of a cDNA Encoding Ethylene Receptor That Expresses in Phalaenopsis Petals (Accession Number AF055894) (PGR99-047)
 JOURNAL Plant Physiol. 119 (4), 1567 (1999)
 REFERENCE 2 (residues 1 to 633)
 AUTHORS Huang, P.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAR-1998) Horticulture, National Taiwan University, No.1, Section 4, Roosevelt Rd, Taipei, Taiwan 10617, Republic of China
 COMMENT Method: conceptual translation.
 FEATURES
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 /organism="Phalaenopsis sp. 'True Lady'"
 /strain="True Lady"
 /db_xref="taxon:55299"
 /clone="pER120"
 /tissue_type="petal"
 /dev_stage="one day after pollination"
 Protein 1..633
 /product="ethylene receptor homolog"
 CDS 1..633
 /gene="Petr1"
 /coded_by="AF055894.1:129..2030"
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 61 fivlcgathl inlwtftmhs rtlaivmtva kvstavvsca talmlvhiip dlsvktrel
 121 flrnkaeeld kemglirtqe etgrhvrmlt heirstldrh tilrttlvel grtldlaeca
 181 lwmpsrvtgln lqlshtlnnq ipvgsvvsin lpvvnqvfnv sravriphtc qlarfqphtg
 241 ryvppevvav rvpllhlsnf qindwpelsa knfavmvlml psdsarkwhv yelevvevva
 301 dqvalvalsha aileesmrar dqlmdqnvla dlarreaema irarndflav mnhemrtpmh
 361 aialsslll eteltpeqrl mvetilkssn llatlindvl dlskledgsf elevtvfnlh
 421 tvfrevvnli kpiaavkklv livslspdlp scavgdekrl mqtmlnvvgv avkftkegsi
 481 sitasiakpd slrdprdpf ypipsgdhfy lrvqikdtgc gispqelphl ftkfahagng
 541 sdkgyngsgl glaickrfvn lmkghiwles evlgkgctti fivkvgised pahryqhkl
 601 ppiragqsea dafgskrtpt dliplknryq rsl

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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search: Protein		for				Go	Clear
Limits		Index		History		Clipboard	
Display: Default View		as HTML		Save		Add to Clipboard	

☐ 1: BAA37129 **gibberelin 3beta-hydroxylase** [Lactuca sativa] BLink, PubMed, Related Sequences, Nucleotide, Taxonom

LOCUS BAA37129 363 aa PLN 05-FEB-1999
 DEFINITION gibberelin 3beta-hydroxylase [Lactuca sativa].
 ACCESSION BAA37129
 PID g4164145
 VERSION BAA37129.1 GI:4164145
 DBSOURCE locus AB012205 accession AB012205.1
 KEYWORDS .
 SOURCE Lactuca sativa.
 ORGANISM Lactuca sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllphytes; Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; Asterales; Asteraceae; Lactuca.

REFERENCE 1 (residues 1 to 363)
 AUTHORS Toyomasu, T.
 TITLE Direct Submission
 JOURNAL Submitted (16-MAR-1998) Tomonobu Toyomasu, Yamagata University, Faculty of Agriculture; Wakaba-cho 1-23, Tsuruoka, Yamagata 997-8555, Japan (E-mail:toyomasu@tds1.tr.yamagata-u.ac.jp, Tel:81-0235-28-2861, Fax:81-0235-28-2812)

REFERENCE 2 (sites)
 AUTHORS Toyomasu, T., Kawaide, H., Mitsunashi, W., Inoue, Y. and Kamiya, Y.
 TITLE Phytochrome regulates gibberellin biosynthesis during germination of photoblastic lettuce seeds
 JOURNAL Plant Physiol. 118 (4), 1517-1523 (1998)
 MEDLINE 99063790

FEATURES Location/Qualifiers
 source 1..363
 /organism="Lactuca sativa"
 /db_xref="taxon:4236"
 /tissue_type="seed"
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 /function="2-oxoglutarate-dependent dioxygenase"
 /product="gibberelin 3beta-hydroxylase"
 CDS 1..363
 /gene="Ls3h1"
 /coded_by="AB012205.1:35..1126"

ORIGIN
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 61 amklvghack twgvfqvtnh gvptnlleem eaagrklfal piqqklkaar apdgvsygyv
 121 arissffpkl mwsegftiig spyeharklw pnrysrfdv iegykhemnn laqrlmwlm
 181 gslgvttedv kwdgsqgscp alqlnsypac pdpdramgla ahtdstllti lyqnntsglq
 241 ahregagwvt vppipgalvv nvgdllhils nglypsvlhr amvnrtqhr1 svaylygpps
 301 nvqisplskl tdhvhpplyr pvtwseylgt kakhfnkals svrlcvplng fvdandhsqv
 361 pvg

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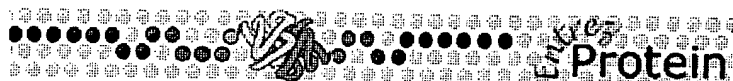
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Limits		Index	History	Clipboard			
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: CAA74331 **gibberellin 20-oxidase** BLINK, Related Sequences, Nucleotide, Taxonomy
[Triticum aestivum]

LOCUS CAA74331 365 aa PLN 25-JUN-1997
 DEFINITION gibberellin 20-oxidase [Triticum aestivum].
 ACCESSION CAA74331
 PID g2222798
 VERSION CAA74331.1 GI:2222798
 DBSOURCE embl locus TAY14008, accession Y14008.1
 KEYWORDS .
 SOURCE Triticum aestivum.
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
 Poaceae; Triticum.
 REFERENCE 1 (residues 1 to 365)
 AUTHORS Appleford, N.E.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-1997) Appleford N.E., Plant Sciences, IACR-Long
 Ashton Research Station, Dept. of Agricultural Sciences, University
 of Bristol, Long Ashton, Bristol. BS18 9AF UK
 REFERENCE 2 (residues 1 to 365)
 AUTHORS Appleford, N.E.J.
 TITLE Cloning and characterisation of cDNAs encoding gibberellin
 20-oxidase from wheat (Triticum aestivum L.)
 JOURNAL Unpublished
 FEATURES Location/Qualifiers
 source 1..365
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 /strain="Rht3"
 /cultivar="Maris Huntsman"
 /db_xref="taxon:4565"
 /clone="S39A"
 /tissue_type="scutellum"
 /clone_lib="LambdaZapScut"
 /dev_stage="germinating grain 3 days at 25 degrees C"
 Protein 1..365
 /product="gibberellin 20-oxidase"
 CDS 1..365
 /db_xref="SPTREMBL:O04706"
 /coded_by="Y14008.1:176..1273"

ORIGIN
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 121 grfasklpwk etlsfrscps dpalvvdv yiv atlgedhrrl gevyarycse msrlsleime
 181 vlgeslgvgr ahyrrffegn dsimrlnyyp pcqrpmetlg tgphcdptsl tilhqdnvvg
 241 lqvhtegrwr sirpradafv vnigdtfmal sngryksclh ravvnskvpr kslafflcpe
 301 mdkvvappgt lvdaanpray pdftwrslll ftqkhyradm ktlevfsswi vqqqqgqlp
 361 plash

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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM		
Search		Protein	for					Go	Clear
Limits		Index		History		Clipboard			
Display	Default View	as	HTML	Save	Add to Clipboard				

☐ 1: AAB67838 **gibberellin 20-oxidase**
[*Pisum sativum*]

BLink, Related Sequences, Nucleotide, Taxonomy

LOCUS AAB67838 379 aa PLN 28-AUG-1997
 DEFINITION gibberellin 20-oxidase [*Pisum sativum*].
 ACCESSION AAB67838
 PID g1381673
 VERSION AAB67838.1 GI:1381673
 DBSOURCE locus PSU58830 accession U58830.1
 KEYWORDS .
 SOURCE pea.
 ORGANISM *Pisum sativum*
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 Fabales; Fabaceae; Papilionoideae; *Pisum*.
 REFERENCE 1 (residues 1 to 379)
 AUTHORS Lester,D.R., Ross,J.J., Ait-Ali,T., Martin,D.N. and Reid,J.B.
 TITLE A gibberellin 20-oxidase cDNA (Accession no. U58830) from pea seed
 (PGR96-050)
 JOURNAL Plant Physiol. 111, 1353 (1996)
 REFERENCE 2 (residues 1 to 379)
 AUTHORS Lester,D.R., Ross,J.J., Ait-Ali,T., Martin,D.N. and Reid,J.B.
 TITLE Direct Submission
 JOURNAL Submitted (21-MAY-1996) Plant Science, University of Tasmania,
 Churchill Avenue, Hobart, TAS 7005, Australia
 COMMENT Method: conceptual translation supplied by author.
 FEATURES
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 source 1..379
 /organism="Pisum sativum"
 /strain="Torsdag"
 /strain="Torsdag"
 /db_xref="taxon:3888"
 Protein 1..379
 /product="gibberellin 20-oxidase"
 /name="2-oxoglutarate-dependent dioxygenase"
 CDS 1..379
 /coded_by="U58830.1:221..1360"
 ORIGIN
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 61 vppidlkafl sddpksisna cskvnhackk hgfflvvnhg vdnkلياqah klvdeffcmq
 121 lsekqraqrk igehegyans figrfssklp wketlsfrys adescrtved yfvnimgedf
 181 rqfgivyqky ceamsnlsig imellgmslg vgkeyfreff egnesvmrln ypppcknpdl
 241 afgtgphcdp tsiltihqdq veglqvlvdg iwhsvvpked afvvnigdtf malsngmfks
 301 clhraivndk ivrkslaffl cpnedkivtp pkelidkenp rkypnftwps lleftqkhyr
 361 adertldafs mwlqekttt
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PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

Search Protein ☐ for [Go] [Clear]

Limits Index History Clipboard

Display Default View ☐ as HTML ☐ Save Add to Clipboard

☐ 1: CAB45891 putative protein BLink, Related Sequences, Nucleotide, Taxonomy
[Arabidopsis thaliana]

LOCUS CAB45891 363 aa PLN 24-JUN-1999

DEFINITION putative protein [Arabidopsis thaliana].

ACCESSION CAB45891

PID g5262786

VERSION CAB45891.1 GI:5262786

DBSOURCE embl locus ATT13K14, accession AL080282.1

KEYWORDS .

SOURCE thale cress.

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
Brassicaceae; Arabidopsis.

REFERENCE 1 (residues 1 to 363)

AUTHORS Bevan, M., Pohl, T., Weizenegger, T., Bancroft, I., Mewes, H.W.,
Mayer, K.F.X., Lemcke, K. and Schueller, C.

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 363)

AUTHORS EU Arabidopsis sequencing, project.

TITLE Direct Submission

JOURNAL Submitted (24-JUN-1999) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
schueller@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbsrc.ac.uk

COMMENT Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.

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/variety="Columbia"
/db_xref="taxon:3702"
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ORIGIN

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181 ggyyskllqe ydailsssl sdelssissq eainvsiqpi qiivasnaqq shilasshtv
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301 dlevllrdgf eqkllqkvii evlpewstk d erqiasmkwl eskhvkdlqs kqlggsvlle

361 gyf

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[NCBI](#) | [NLM](#) | [NIH](#)



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
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Limits		Index		History		Clipboard	
Display	Default View	as	HTML	Save	Add to Clipboard		

1: AAB72193 ethylene responsive factor BLink, Related Sequences, Nucleotide, Taxonomy [Oryza sativa]

LOCUS AAB72193 636 aa PLN 06-OCT-1997
 DEFINITION ethylene responsive factor [Oryza sativa].
 ACCESSION AAB72193
 PID g2281705
 VERSION AAB72193.1 GI:2281705
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 KEYWORDS .
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
 Oryza.
 REFERENCE 1 (residues 1 to 636)
 AUTHORS Yau,C.P. and Yip,W.K.
 TITLE Nucleotide sequence of a full-length cDNA encoding an ethylene
 receptor from rice (Accession No. AF013979) (PGR97-134)
 JOURNAL Plant Physiol. 115, 315 (1997)
 REFERENCE 2 (residues 1 to 636)
 AUTHORS Yau,C.P. and Yip,W.K.
 TITLE Direct Submission
 JOURNAL Submitted (14-JUL-1997) Botany, University of Hong Kong, Pokfulam
 Road, Hong Kong, Hong Kong
 COMMENT Method: conceptual translation supplied by author.
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 121 flknkaeqld remglirtqe etgrhvrmlt heirstldrh tilkttlvel ggtlgleeca
 181 lwmpsrsgss lqlshtlrhq itvgstvsin lpvvnqvffs nräiiphts plarirplag
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 361 aialsslll eteltpegrl mvetvlkssn llatlindvl dlskledgs1 eleikafnlh
 421 avfkevmsfi kpiaaikrls vsvmlapdlp lcaigdekrl mqtlnisgn avkftkeghi
 481 tlvasvvkad slrefrtpdf hptasddnfy lkvqikdtgc gispqdlpqv ftkfpqsqpg
 541 gnrgysgsgl glaickrfvt lmgghiwlds egtgrgctvt fviqlgicdn tnayqqklip
 601 lvwpssgdad fvgpvpnapn eekgqaslks ryqrsi

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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search	Protein	for					Go
Limits		Index		History		Clipboard	
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: **AAD03598 ethylene response sensor** BLink, Related Sequences, Nucleotide, Taxonomy
[Vigna radiata]

LOCUS AAD03598 636 aa PLN 10-JAN-1999
 DEFINITION ethylene response sensor [Vigna radiata].
 ACCESSION AAD03598
 PID g4138853
 VERSION AAD03598.1 GI:4138853
 DBSOURCE locus AF098272 accession AF098272.1
 KEYWORDS .
 SOURCE mung bean.
 ORGANISM Vigna radiata
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 Fabales; Fabaceae; Papilionoideae; Vigna.
 REFERENCE 1 (residues 1 to 636)
 AUTHORS Kim, J.H., Lee, J.-H., Joo, S. and Kim, W.T.
 TITLE Structure of a cDNA encoding an ERS1 homolog and induction of its
 mRNA by ethylene in mung bean seedlings
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 636)
 AUTHORS Kim, J.H., Lee, J.-H., Joo, S. and Kim, W.T.
 TITLE Direct Submission
 JOURNAL Submitted (08-OCT-1998) Biology, Yonsei University, Sinchon dong
 134, Seoul 120-749, Korea
 COMMENT Method: conceptual translation supplied by author.
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 Protein 1..636
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 CDS 1..636
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481 vsirasvakp eslqdrppe fyptssdghf yirvqvkdsg cgippqdiph lftkfaqsrs
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Limits	Index	History	Clipboard				
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: CAB51211 putative protein
[Arabidopsis thaliana]

BLink, Related Sequences, Nucleotide, Taxonomy

LOCUS CAB51211 599 aa PLN 19-JUL-1999
 DEFINITION putative protein [Arabidopsis thaliana].
 ACCESSION CAB51211
 PID g5541706
 VERSION CAB51211.1 GI:5541706
 DBSOURCE embl locus ATT21L8, accession AL096860.1
 KEYWORDS .
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
 Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 599)
 AUTHORS Choisine, N., Robert, C., Brottier, P., Wincker, P., Cattolico, L.,
 Artiguenave, F., Saurin, W., Weissenbach, J., Mewes, H.W.,
 Mayer, K.F.X., Lemcke, K., Schueller, C., Quetier, F. and Salanoubat, M.
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 599)
 AUTHORS EU Arabidopsis sequencing, project.
 TITLE Direct Submission
 JOURNAL Submitted (19-JUL-1999) MIPS, at the Max-Planck-Institut fuer
 Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
 schuelle@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project
 Coordinator: Marcel Salanoubat and Francis Quetier, Groupement
 d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue
 Gaston Cremieux, BP191, 91006 Evry Cedex, France;
 http://www.genoscope.cns.fr
 COMMENT Information on performance of analysis and a more detailed
 annotation of this entry and other sequences of chromosomes 3, 4
 and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.
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 121 giervvvgir hplqhlrgsa irelrshgie vnvlgedfes kvledarksc llvnaplihr

181 acsrvpfsvl kyamtldgki aassghaawi ssklsrtrvf elrggsdavi vggntvrqdd
241 prltarhggg htptrivmtg sldlpekanl wdvsevestiv vtqrgarksf qkllaskgve
301 vvefdmlnpr evmeyfhlg ylsilwecgg tlaasaiss vihkvvafva pkiiggskap
361 spvgdlgmve mtqalnldv cyeqvgpdml vsgflqpdp llpvipseda tveidpsvdp
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481 pkaydcveki rtarspeaaa ligrstlrqk pelvrndwed vkievmykal kckfstyphl
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Page 1 of 1



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search		Protein	for		Go	Clear	
Limits		Index		History		Clipboard	
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: T09672 **ent-kaurene synthase B (EC 2.5.1.-) - winter squash** BLink, PubMed, Related Sequences, Taxonomy

LOCUS T09672 789 aa PLN 21-JUL-2000
 DEFINITION ent-kaurene synthase B (EC 2.5.1.-) - winter squash.
 ACCESSION T09672
 PID g7484763
 VERSION T09672 GI:7484763
 DBSOURCE pir: locus T09672;
 summary: #length 789 #molecular-weight 89361 #checksum 4319;
 PIR dates: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000.
 KEYWORDS transferase.
 SOURCE winter squash.
 ORGANISM Cucurbita maxima
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
 REFERENCE 1 (residues 1 to 789)
 AUTHORS Yamaguchi, S., Saito, T., Abe, H., Yamane, H., Murofushi, N. and Kamiya, Y.
 TITLE Molecular cloning and characterization of a cDNA encoding the gibberellin biosynthetic enzyme ent-kaurene synthase B from pumpkin (Cucurbita maxima L.)
 JOURNAL Plant J. 10 (2), 203-213 (1996)
 MEDLINE 96367664
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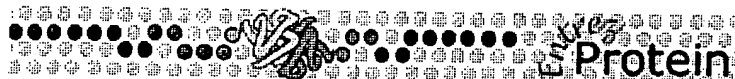
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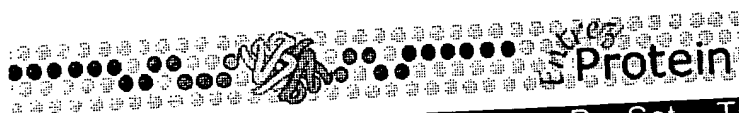
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☐ 1: **BAA34124 3b-hydroxylase** BLink, Related Sequences, Nucleotide, Taxonomy
[Lycopersicon esculentum]

LOCUS BAA34124 373 aa PLN 23-MAY-2000
 DEFINITION 3b-hydroxylase [Lycopersicon esculentum].
 ACCESSION BAA34124
 PID g3834350
 VERSION BAA34124.1 GI:3834350
 DBSOURCE locus AB010991 accession AB010991.1
 KEYWORDS .
 SOURCE tomato.
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
 Solanaceae; Solanum; Lycopersicon.
 REFERENCE 1 (sites)
 AUTHORS Yang,Y.Y., Rebers,M., Toyomasu,T., Kawaide,H., Kaneta,T. and
 Kamiya,Y.
 TITLE Cloning of two cDNAs encoding gibberellin 3beta-hydroxylase
 (Accession No. AB010991, AB010992) of tomato (Solanum lycopersicum
 L.) seedlings (PGR98-200)
 JOURNAL Plant Physiol. 118, 1534 (1998)
 REFERENCE 2 (residues 1 to 373)
 AUTHORS Yang,Y.Y., Kaneta,T. and Kamiya,Y.
 TITLE Direct Submission
 JOURNAL Submitted (08-FEB-1998) Yuji Kamiya, Institute of Physical and
 Chemical Research (RIKEN), Plant Functions Laboratory; Hirosawa
 2-1, Wako, Saitama 351-0198, Japan
 (E-mail:ykamiya@postman.riken.go.jp, Tel:81-48-462-9375,
 Fax:81-48-462-4691)
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 CDS 1..373
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 241 lhqntsglq vyqegnwig vppipgalvv nigdllhils ngsypsvlhr avvnrttryl
 301 svaylygpps gvrvsplskl vdhrhplyr avtwseylgt kakyfdkals svrlcvplng
 361 ftdakdhkgv qvg
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PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

Search Protein for [] Limits Index History Clipboard

Display Default View [] as HTML [] Save Add to Clipboard

BLink, Related Sequences, Nucleotide, Taxonomy

☐ 1: AAD22645 putative
P-glycoprotein-like protein
[*Arabidopsis thaliana*]

LOCUS AC007138_9 1230 aa PLN 01-APR-1999
DEFINITION putative P-glycoprotein-like protein [*Arabidopsis thaliana*].
ACCESSION AAD22645
PID g4558552
VERSION AAD22645.1 GI:4558552
DBSOURCE locus AC007138 accession AC007138.1
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ORGANISM *Arabidopsis thaliana*
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (residues 1 to 1230)
AUTHORS Huang, E.N., Nascimento, L., de la Bastide, M., Habermann, K.,
Vil, M.D., Preston, R.R., Spiegel, L.A., See, L.H., Shah, R., Matero, A.,
O'Shaughnessy, A., Rodriguez, M., Shekher, M., Swaby, I., Schutz, K.,
Parnell, L.D., Dedhia, N.N. and McCombie, W.R.
TITLE *Arabidopsis thaliana* BAC T7B11 from chromosome IV near 10 cM
JOURNAL Unpublished

REFERENCE 2 (residues 1 to 1230)
AUTHORS Huang, E.N., Nascimento, L., de la Bastide, M., Habermann, K.,
Vil, M.D., Preston, R.R., Spiegel, L.A., See, L.H., Shah, R., Matero, A.,
O'Shaughnessy, A., Rodriguez, M., Shekher, M., Swaby, I., Schutz, K.,
Parnell, L.D., Dedhia, N.N. and McCombie, W.R.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-1999) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724

REFERENCE 3 (residues 1 to 1230)
AUTHORS Parnell, L.D.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1999) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724

REMARK *Arabidopsis thaliana* BAC T7B11 from chromosome IV near 9.5 cM
COMMENT Method: conceptual translation supplied by author.
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AC007138.1:31827..32626,AC007138.1:32715..32953,
AC007138.1:33051..33272,AC007138.1:33354..33529,
AC007138.1:33605..33659,AC007138.1:33745..33963))"
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GenBank accession number Y15990; similar to mdr multi-drug
resistance proteins; functional catalog ID=07.28"

ORIGIN

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241 linlayksnv kqgfvtglgl gvmflvffst yalgtwfgge milrkgytgg avinvmvtvv
301 sssialgqas pcltaftagk aaaykmfeti ereplidtdf lngkvledir geielrdvcf
361 syparpkeev fggfsl lips gtttalvges gsgkstvisl ierfydpnsg qvlidgvdlk
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541 rttvivahrl stvrnadiia vihrgekivee gshsellkdh egaysqllrl qeinkeskrl
601 eisdgsissg ssrgnnstrq ddsfsvlgl lagqdstkms qelsqkvsft riaalnkepi
661 pililgtlv ggrlirris mcfekvvhme vgwfdpgns sgamgarlsa daalirtlv
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781 eeasqvanda vgsirtvasf caeekvmemy kkrceatiks gikqglisgv gfgisffvly
841 svyascfyvg arlvkagrtn fndvfqvfla ltltavgisq assfapdssk gkgaavsifr
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Search	Protein	for					Go Clear
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☐ 1: [AAF71978](#) Putative ABC transporter BLINK, Related Sequences, Nucleotide, Taxonomy
[Arabidopsis thaliana]

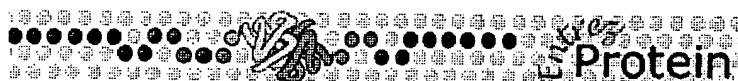
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 DEFINITION Putative ABC transporter [Arabidopsis thaliana].
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 Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 1423)
 AUTHORS Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
 Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P.,
 Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S.,
 Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskaia, V.S.,
 Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 1423)
 AUTHORS Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
 Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P.,
 Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S.,
 Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V.,
 Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
 TITLE Direct Submission
 JOURNAL Submitted (12-NOV-1999) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 REFERENCE 3 (residues 1 to 1423)
 AUTHORS Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
 Altafi, H., Nguyen, M., Lam, B., Southwick, A., Ecker, J., Theologis, A.
 and Davis, R.W.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAY-2000) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 COMMENT Method: conceptual translation supplied by author.
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ORIGIN

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☐ 1: AAB63643 **ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]** [BLink, Related Sequences, Nucleotide, Taxonomy](#)

LOCUS AAB63643 1416 aa PLN 22-JUL-1997
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 PID g2062169
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 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 1416)
 AUTHORS Rounsley, S.D., Lin, X., Ketchum, K.A., Phillips, C.A., Brandon, R.C.,
 Fuhrmann, J.L., White, O., Kerlavage, A.R., Adams, M.D.,
 Somerville, C.R. and Venter, J.C.
 TITLE Arabidopsis thaliana chromosome III BAC T02004 genomic sequence
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 1416)
 AUTHORS Rounsley, S.D.
 TITLE Direct Submission
 JOURNAL Submitted (22-APR-1997) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 REFERENCE 3 (residues 1 to 1416)
 AUTHORS Rounsley, S.D.
 TITLE Direct Submission
 JOURNAL Submitted (22-JUL-1997) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 COMMENT Method: conceptual translation.
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☐ 1: AAD24623 **putative** BLink, PubMed, Related Sequences, Nucleotide, Genome, Tax
ABC
transporter
[Arabidopsis
thaliana]

LOCUS AC006919_2 1450 aa PLN 05-APR-2000
 DEFINITION putative ABC transporter [Arabidopsis thaliana].
 ACCESSION AAD24623
 PID g4581139
 VERSION AAD24623.1 GI:4581139
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 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 1450)
 AUTHORS Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D.,
 Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E.,
 Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M.,
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 Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H.,
 Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D.,
 Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
 Venter,J.C.
 TITLE Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana
 JOURNAL Nature 402 (6763), 761-768 (1999)
 MEDLINE 20083487
 PUBMED 10617197
 REFERENCE 2 (residues 1 to 1450)
 AUTHORS Lin,X.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 COMMENT Method: conceptual translation.
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☐ 1: AAF19673 **F1N19.11 [Arabidopsis thaliana]** BLink, Related Sequences, Nucleotide, Taxonomy

LOCUS AC009519.7 1270 aa PLN 11-OCT-2000
 DEFINITION F1N19.11 [Arabidopsis thaliana].
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 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (residues 1 to 1270)
 AUTHORS Chao,Q., Brooks,S., Buehler,E., Johnson-Hopson,C., Khan,S., Kim,C.,
 Shinn,P., Tambunga,G., Altafi,H., Bei,Q., Chin,C., Chiou,J.,
 Choi,E., Conn,L., Conway,A., Gonzales,A., Hansen,N., Howng,B.,
 Koo,T., Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S.,
 Mukharsky,N., Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J.,
 Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G.,
 Federspiel,N.A., Theologis,A. and Ecker,J.R.
 TITLE Genomic sequence for Arabidopsis thaliana BAC F1N19 from chromosome
 I
 JOURNAL Unpublished

REFERENCE 2 (residues 1 to 1270)
 AUTHORS Ecker,J.R.
 TITLE Direct Submission
 JOURNAL Submitted (26-AUG-1999) Arabidopsis thaliana Genome Center,
 Department of Biology, University of Pennsylvania, 38th Street and
 Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

REFERENCE 3 (residues 1 to 1270)
 AUTHORS Ecker,J.R.
 TITLE Direct Submission
 JOURNAL Submitted (14-OCT-1999) Arabidopsis thaliana Genome Center,
 Department of Biology, University of Pennsylvania, 38th Street and
 Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

REFERENCE 4 (residues 1 to 1270)
 AUTHORS Chao,Q., Brooks,S., Buehler,E., Johnson-Hopson,C., Khan,S., Kim,C.,
 Shinn,P., Altafi,H., Bei,B., Chin,C., Chiou,J., Choi,E., Conn,L.,
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 Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Davis,R.,
 Federspiel,N., Theologis,A. and Ecker,J.
 TITLE Direct Submission
 JOURNAL Submitted (23-DEC-1999) Arabidopsis thaliana Genome Center,
 Department of Biology, University of Pennsylvania, 38th and
 Hamilton Walk, Philadelphia, PA 19104-6018, USA

REFERENCE 5 (residues 1 to 1270)
 AUTHORS Cheuk,R., Shinn,P., Brooks,S., Buehler,E., Chao,Q.,
 Johnson-Hopson,C., Khan,S., Kim,C., Altafi,H., Bei,B., Chin,C.,
 Chiou,J., Choi,E., Conn,L., Conway,A., Gonzalez,A., Hansen,N.,

Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,
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Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M.,
Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.

TITLE Direct Submission
JOURNAL Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, PA 19104-6018, USA

REFERENCE 6 (residues 1 to 1270)
AUTHORS Chao, Q., Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C.,
Shinn, P., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L.,
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Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R.,
Federspiel, N., Theologis, A. and Ecker, J.

TITLE Direct Submission
JOURNAL Submitted (11-OCT-2000) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, PA 19104-6018, USA

COMMENT Method: conceptual translation.
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/note="similar to ABC transporter emb|CAA18386; similar to
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ORIGIN
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601 revysngsff tgfelricfl scvylllqyq qhvaemeaak agmptvsvnh dtgggsaird
661 ihmdnfnvsv ggrdlivdgs itlsfgrhyg lvgrngtgkt tflrymamha iegiptncqi
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1261 dykkllqsst
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[Restrictions on Use](#) | [Write to the HelpDesk](#)
[NCBI](#) | [NLM](#) | [NIH](#)



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search		Protein	for			Go	Clear
Limits		Index		History		Clipboard	
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☐ 1: AAA91256 coded for by C. BLink, PubMed, Related Sequences, Nucleotide, Genome, T
elegans cDNA
yk95g9.3;
Similar to
acyl-CoA
thioesterase
[Caenorhabditis
elegans]

LOCUS AAA91256 343 aa INV 03-MAR-1996
 DEFINITION coded for by C. elegans cDNA yk95g9.3; Similar to acyl-CoA
 thioesterase.
 ACCESSION AAA91256
 PID g1213545
 VERSION AAA91256.1 GI:1213545
 DBSOURCE locus CELF25E2 accession U50197.1
 KEYWORDS .
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (residues 1 to 343)
 AUTHORS Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
 Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
 Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
 Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
 Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
 Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
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 Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonhammer,E.,
 Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
 Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
 Wilkinson-Sproat,J. and Wohldman,P.
 TITLE 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans
 JOURNAL Nature 368 (6466), 32-38 (1994)
 MEDLINE 94150718
 REFERENCE 2 (residues 1 to 343)
 AUTHORS Minx,P. and Le,T.
 TITLE The sequence of C. elegans cosmid F25E2
 JOURNAL Unpublished
 COMMENT Submitted by:
 Genome Sequencing Center
 Department of Genetics, Washington University,
 St. Louis, MO 63110, USA, and
 Sanger Centre, Hinxton Hall
 Cambridge CB10 1RQ, England
 e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
 NEIGHBORING COSMID INFORMATION:
 5' cosmid is T04G9, 650 bp overlap; 3' cosmid is F39H12, 200 bp
 overlap. Actual start of this cosmid is at base position 26996 of
 CELT04G9; actual end is at bp 29780 of CELF25E2.

NOTES:

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation).

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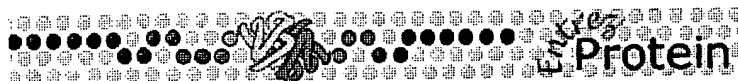
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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search	Protein	for					Go
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Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: NP_005460 peroxisomal BLink, PubMed, Related Sequences, Nucleotide, Taxonomy, Lin
acyl-CoA
thioesterase
[Homo
sapiens]

LOCUS NP_005460 319 aa PRI 01-NOV-2000
 DEFINITION peroxisomal acyl-CoA thioesterase [Homo sapiens].
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 PID g4885565
 VERSION NP_005460.1 GI:4885565
 DBSOURCE REFSEQ: accession NM_005469.1
 KEYWORDS .
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 319)
 AUTHORS Liu, L.X., Margottin, F., Le Gall, S., Schwartz, O., Selig, L.,
 Benarous, R. and Benichou, S.
 TITLE Binding of HIV-1 Nef to a novel thioesterase enzyme correlates with
 Nef-mediated CD4 down-regulation
 JOURNAL J. Biol. Chem. 272 (21), 13779-13785 (1997)
 MEDLINE 97298085
 REFERENCE 2 (residues 1 to 319)
 AUTHORS Watanabe H, Shiratori T, Shoji H, Miyatake S, Okazaki Y, Ikuta K,
 Sato T and Saito T.
 TITLE A novel acyl-CoA thioesterase enhances its enzymatic activity by
 direct binding with HIV Nef
 JOURNAL Biochem. Biophys. Res. Commun. 238 (1), 234-239 (1997)
 MEDLINE 97445158
 PUBMED 9299485
 REFERENCE 3 (residues 1 to 319)
 AUTHORS Jones JM, Nau K, Geraghty MT, Erdmann R and Gould SJ.
 TITLE Identification of peroxisomal acyl-CoA thioesterases in yeast and
 humans
 JOURNAL J. Biol. Chem. 274 (14), 9216-9223 (1999)
 MEDLINE 99194760
 PUBMED 10092594
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
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 CDS 1..319

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 121 ificqasfqg aqpspmqhgf smptvpppee lldcetlidq ylrdpnlqkr yplalnriaa
 181 qevpieikpv npsplsqlqr mepkqmfivr argyigegdm kmhccvaayi sdyaf1gtal
 241 lphqwghkvh fmvsl dhsmw fhapfradhw mlyecespwa ggsrglvhgr vwsqdgvlav
 301 tcaqegvirv kpqvseskr
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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search	Protein	<input checked="" type="checkbox"/> for				Go	Clear
Limits		Index		History		Clipboard	
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1: T03439 probable ethylene-response protein - rice BLink, Related Sequences, Taxonomy

LOCUS T03439 636 aa PLN 24-MAR-1999
 DEFINITION probable ethylene-response protein - rice.
 ACCESSION T03439
 PID g7489538
 VERSION T03439 GI:7489538
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 summary: #length 636 #molecular-weight 70709 #checksum 4061;
 genetic: #gene ERS;
 PIR dates: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999.

KEYWORDS .
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 Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

REFERENCE 1 (residues 1 to 636)
 AUTHORS Yau,C.P. and Yip,W.K.
 TITLE Direct Submission
 JOURNAL Submitted (??-JUL-1997) to the EMBL Data Library

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121 flknkaeqld remglirtqe etgrhvrmlt heirstldrh tilkttlvel ggtlgleeca
181 lwmpsrsgss lqlshlrlhq itvgstvsin lpvvnqvfss nrailiiphs plarirplag
241 ryvppevaav rvpllhlsnf qindwpelsa ksyaimvlml psdsarkwhv helelvevva
301 dqvalvalsha aileesmrar dllmeqnaval dlarreaema irarndflav mnhemrtpmn
361 aialsslll eteltpeqrl mvetvlkssn llatlindvl dlskledgsl eleikafnlh
421 avfkevmsfi kpiaaikrls vsvmlapdlp lcaigdekrl mqtilnisgn avkftkeghi
481 tlvasvkvad slrefrtpdf hptasddnfy lkvqikdtgc gispqdlpqv ftkfpqsqpg
541 gnrgysgsgl glaickrfvt lmgghiwlds egtgrgctvt fviqlgicdn tnayqqkclip
601 lvwpssgdad fvgpvpnapn eekgqaslks ryqrsl

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 NCBI | NLM | NIH



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Search	Protein	for					Go	Clear
Limits		Index	History	Clipboard				
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☐ 1: **AAC79098 putative oxidoreductase** BLink, Related Sequences, Nucleotide, Taxonomy
[Arabidopsis thaliana]

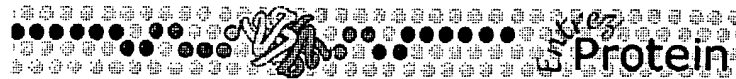
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 DEFINITION putative oxidoreductase [Arabidopsis thaliana].
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 PID g3924597
 VERSION AAC79098.1 GI:3924597
 DBSOURCE locus AF069442 accession AF069442.1
 KEYWORDS .
 SOURCE thale cress.
 ORGANISM *Arabidopsis thaliana*
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 322)
 AUTHORS Parnell,L.D., Gnoj,L., de la Bastide,M., Hameed,A., Habermann,K.,
 Schutz,K., Huang,E., Gottesman,T., Dedhia,N.N. and McCombie,W.R.
 TITLE Genomic sequence of BAC T4I9 from *Arabidopsis thaliana*, Chromosome
 IV, near 16.6 cM
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 322)
 AUTHORS Gnoj,L., Parnell,L.D., de la Bastide,M., Hameed,A., Habermann,K.,
 Schutz,K., Huang,E., Gottesman,T., Dedhia,N.N. and McCombie,W.R.
 TITLE Direct Submission
 JOURNAL Submitted (29-MAY-1998) Lita Annenberg Hazen Genome Sequencing
 Center, Cold Spring Harbor Laboratory, Cold Spring Harbor
 Laboratory, Cold Spring Harbor, NY 11724, USA
 COMMENT Method: conceptual translation supplied by author.
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 20-oxidase, GenBank accession number U58830; similar to O.
 sativa gibberellin C-20 oxidase, GenBank accession number
 U50333; similar to P. vulgaris gibberellin 20-oxidase,
 GenBank accession number U70531; most similar to T4I9.6
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 functional catalog ID=01.20"

ORIGIN

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121 hgnksiseti hlfseqlvel dlmvrrmime sfgienyide hlnstyyltr lmkytsppdd
181 dddddeetkl glrshtdkni itilhqyqvd glevktkddk wikvkpsqds vlvmvgdslc
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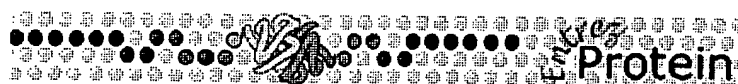
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NCBI | NLM | NIH



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search Protein		for		Go		Clear	
Limits		Index		History		Clipboard	
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: CAB41036 **GA 2-oxidase** BLink, PubMed, Related Sequences, Nucleotide, Taxonomy
[Phaseolus
coccineus]

LOCUS CAB41036 332 aa PLN 20-APR-1999
 DEFINITION GA 2-oxidase [Phaseolus coccineus].
 ACCESSION CAB41036
 PID g4678586
 VERSION CAB41036.1 GI:4678586
 DBSOURCE embl locus PC0132438, accession AJ132438.1
 KEYWORDS .
 SOURCE Phaseolus coccineus.
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 eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
 Phaseolus.
 REFERENCE 1 (residues 1 to 332)
 AUTHORS Thomas, S.G., Phillips, A.L. and Hedden, P.
 TITLE Molecular cloning and functional expression of gibberellin 2-
 oxidases, multifunctional enzymes involved in gibberellin
 deactivation
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (8), 4698-4703 (1999)
 MEDLINE 99218343
 REFERENCE 2 (residues 1 to 332)
 AUTHORS Phillips, A.L.
 TITLE Direct Submission
 JOURNAL Submitted (18-JAN-1999) Phillips A.L., Plant Sciences, IACR Long
 Ashton Research Station, Long Ashton Research Station, Bristol,
 BS41 9AF, UK
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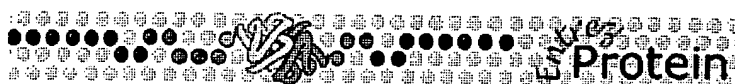
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☐ 1: T06990 **probable giberellin 3beta-dioxygenase (EC BLink, Related Sequences, Taxonomy 1.14.11.15) - wheat**

LOCUS T06990 365 aa PLN 20-JUN-2000
 DEFINITION probable giberellin 3beta-dioxygenase (EC 1.14.11.15) - wheat.
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 PID g7433220
 VERSION T06990 GI:7433220
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 summary: #length 365 #molecular-weight 40737 #checksum 4634;
 superfamily: 1-aminocyclopropane-1-carboxylate oxidase;
 PIR dates: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Jun-2000.
 KEYWORDS ascorbic acid; oxidoreductase; seed.
 SOURCE bread wheat.
 ORGANISM *Triticum aestivum*
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
 REFERENCE 1 (residues 1 to 365)
 AUTHORS Appleford, N.E.
 TITLE Direct Submission
 JOURNAL Submitted (??-JUN-1997) to the EMBL Data Library
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 121 grfasklpwk etlsfrscps dpalvvdvdyiv atlgedhrrl gevyarycse msrlsleime
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Protein

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

Search: for

☐ 1: AAD52015 unknown [Pisum sativum] BLink, Related Sequences, Nucleotide, Taxonomy

LOCUS AF082862.1 134 aa PLN 01-SEP-1999
 DEFINITION unknown [Pisum sativum].
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 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 Fabales; Fabaceae; Papilionoideae; Pisum.
 REFERENCE 1 (residues 1 to 134)
 AUTHORS MacKenzie-Hose, A.K., Lester, D.R. and Ross, J.J.
 TITLE Seeds, GAs and biosynthesis
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 134)
 AUTHORS MacKenzie-Hose, A.K., Lester, D.R. and Ross, J.J.
 TITLE Direct Submission
 JOURNAL Submitted (07-AUG-1998) Plant Science, University of Tasmania, GPO
 Box 252-55, Hobart, Tas 7005, Australia
 COMMENT Method: conceptual translation.
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☐ PubMed ☐ Nucleotide ☐ Protein ☐ Genome ☐ Structure ☐ PopSet ☐ Taxonomy ☐ OMIM

Search Protein ☐ for

☐ 1: CAB75931 **multi resistance protein** BLink, Related Sequences, Nucleotide, Taxonomy
homolog [Arabidopsis thaliana]

LOCUS CAB75931 1490 aa PLN 23-FEB-2000
 DEFINITION multi resistance protein homolog [Arabidopsis thaliana].
 ACCESSION CAB75931
 PID g7076769
 VERSION CAB75931.1 GI:7076769
 DBSOURCE embl locus ATT209, accession AL138658.1
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 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 Arabidopsis.

REFERENCE 1 (residues 1 to 1490)
 AUTHORS Nyakatura,G., Fartmann,B., Dauner,D., Sterr,W., Holland,R.,
 Weichselgartner,M., Mewes,H.W., Lemcke,K., Mayer,K.F.X., Quetier,F.
 and Salanoubat,M.

JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 1490)
 AUTHORS EU Arabidopsis sequencing,project.
 TITLE Direct Submission
 JOURNAL Submitted (23-FEB-2000) MIPS, at the Max-Planck-Institut fuer
 Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
 lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project
 Coordinator: Marcel Salanoubat and Francis Quetier, Groupement
 d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue
 Gaston Cremieux, BP191, 91006 Evry Cedex, France;
<http://www.genoscope.cns.fr>

COMMENT Information on performance of analysis and a more detailed
 annotation of this entry and other sequences of chromosomes 3, 4
 and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.

FEATURES Location/Qualifiers
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 /variety="Columbia"
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 /chromosome="3"
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 CDS 1..1490
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 AL138658.1:61471..61710,AL138658.1:61800..61863,
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 AL138658.1:62631..62925,AL138658.1:63056..63172,
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 AL138658.1:64169..66528,AL138658.1:66608..66632)))"
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 Arabidopsis thaliana, EMBL:ATMRPPROT; Contains ABC
 transporters family signature AA755-769;ATP/GTP-binding

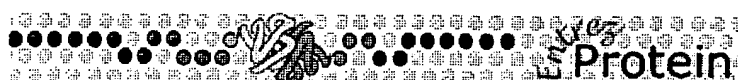
site motif A (P-loop) AA196-203;ATP/GTP-binding site motif
A (P-loop) AA665-672;ATP/GTP-binding site motif A (P-loop)
AA1273-1280;Prokaryotic membrane lipoprotein lipid
attachment site AA459-469;Prokaryotic membrane lipoprotein
lipid attachment site AA935-945"

ORIGIN

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121 aevsqsfswl fvsvvvkvir errlvkfpwm lrswwlcsfi lsfsfdahfi takheplef
181 dyadltglla slfillavsir gktgfhles sgnteplllg dqteqnkkds ysssspygna
241 tlfqritfsw inplfslgyk rplekddvdp idvkdsarfc shafdqklkt tkekegpna
301 ffynsvlryv wrkaainavf avvnastayi gpylindfve flsekqsqsl nhgyllalqf
361 ltakivetvt qrqwifgarq lglrlraali shiyqkglvl ssqsrqshts geinymysvd
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481 qsdimnakdd rmkatseilk nmkilklqaw dnqflnkvkt lrkkeydclw kslrlqafft
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721 sekyertvka calikdfelf sngdlteige rginmssggqk qriqiaravy qnadiylldd
781 pfsavdahtg relfedclmg ilkdktvlyv thqveflpaa dlilvmqngr vmqagkfeel
841 lkqnigfevl vgahnealds ilsiekssrn fkegskddta siaeslqthc dsehnisten
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1201 enkmisveri lqyskipsea plvidghrpl dnwvngvsiv frdlqvryae hfpavlkmit
1261 cefpggkkig vvgrtgsgks tliqalfriw epsqgtivid nvditkighl dlrsrlgiip
1321 qdpalfdgti rlnldplaqy tdheiweaid kcqlgdvira kderldatvv engenwsvgq
1381 rqlvclgrvl lkksnilvld eatasvdsat dgviqkiing efkdrtvvti ahrihtvies
1441 dlvlvlsgdr iaefdspakl lqredsffsk likeyslrn hfagsndlls
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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search [Protein] for				[Go] [Clear]			
Limits		Index		History		Clipboard	
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: CAA05625 **AtMRP4** BLink, PubMed, Related Sequences, Nucleotide, Taxonomy
[Arabidopsis thaliana]

LOCUS CAA05625 1516 aa PLN 11-AUG-1998
 DEFINITION AtMRP4 [Arabidopsis thaliana].
 ACCESSION CAA05625
 PID g2959767
 VERSION CAA05625.1 GI:2959767
 DBSOURCE embl locus ATDNAMRP4, accession AJ002584.1
 KEYWORDS .
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 euphyllphytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 Rosidae; Capparales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 1516)
 AUTHORS Sanchez-Fernandez, R.
 TITLE Direct Submission
 JOURNAL Submitted (05-NOV-1997) Sanchez-Fernandez R., Department of
 Genetics, University of Gent (VIB), K.L. Ledeganckstraat 35, 9000
 Gent, BELGIUM
 REFERENCE 2 (residues 1 to 1516)
 AUTHORS Sanchez-Fernandez, R., Ardiles-Diaz, W., Van Montagu, M., Inze, D. and
 May, M. J.
 TITLE Cloning and expression analyses of AtMRP4, a novel MRP-like gene
 from Arabidopsis thaliana
 JOURNAL Mol. Gen. Genet. 258 (6), 655-662 (1998)
 MEDLINE 98334109
 FEATURES
 source Location/Qualifiers
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 vacuole"
 /product="AtMRP4"
 CDS 1..1516
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ORIGIN

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241 vsveksdnvs lyasavfsk tfwlwmnp1l skgykspltl eqvptlspeh kaerlallfe
301 sswpkpsens shpirttllr cfwkeilfta ilaivrlgvm yvgpvliqsf vdfitsgkrss
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601 smislsqami slgrldsymb skelsedave ralgcdgnta vevrdgsfsw ddednepals
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901 esphlsdlnd ehiksflgsh ivedgsklik eeeretgqvs lgvykqycte aygwwgivlv
961 lffs1twqgs lmasdywlay etsaknaisf dasvfilgyv iialvsivlv sirsyvthl
1021 glktaqiffr qilnsilhap msffdt1tspg rilsrastdq tnvdilipfm lglvvsmytt
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1501 lfaalvqeya lrsagi
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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search Protein		for		Go		Clear	
Limits		Index		History		Clipboard	
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: AAC49791 MRP-like ABC

transporter [Arabidopsis thaliana]

BLink, Related Sequences, Nucleotide, Taxonomy

LOCUS AAC49791 1515 aa PLN 09-AUG-1997
 DEFINITION MRP-like ABC transporter [Arabidopsis thaliana].
 ACCESSION AAC49791
 PID g2316016
 VERSION AAC49791.1 GI:2316016
 DBSOURCE locus ATU92650 accession U92650.1
 KEYWORDS .
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 1515)
 AUTHORS Tommasini,R., Vogt,E., Schmid,J., Fromentau,M., Amrhein,N. and Martinoia,E.
 TITLE Direct Submission
 JOURNAL Submitted (10-MAR-1997) Institut fuer Pflanzenwissenschaften, ETH Zuerich, Universitaetstrasse 2, Zuerich 8092, Switzerland
 COMMENT Method: conceptual translation supplied by author.
 FEATURES
 source 1..1515
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 /strain="Columbia"
 /db_xref="taxon:3702"
 Protein 1..1515
 /product="MRP-like ABC transporter"
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 CDS 1..1515
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301 dggersgvtt fklikalyft aqweilvtaf fafiyvtasy vgpalditfv qylngrrqyn
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421 geiinfmtdv aerignfswy mhdpmwvllq vglalwilyr nlglasiaal vatiivmlin
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1501 klvaeytsrs sssfd
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☐ 1: T06165 multidrug resistance protein 1 homolog - barley

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

Search: Protein ☒ for Limits Index History Clipboard

Display Default View ☒ as HTML ☒ Save Add to Clipboard

BLink, PubMed, Related Sequences, Taxonomy

LOCUS T06165 1232 aa PLN 21-JUL-2000
 DEFINITION multidrug resistance protein 1 homolog - barley.
 ACCESSION T06165
 PID g7442649
 VERSION T06165 GI:7442649
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 superfamily: multidrug resistance protein; ATP-binding cassette
 homology;
 PIR dates: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change
 21-Jul-2000.

KEYWORDS
 SOURCE
 ORGANISM *Hordeum vulgare*
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.

REFERENCE
 AUTHORS Davies, T.G., Theodoulou, F.L., Hallahan, D.L. and Forde, B.G.
 TITLE Cloning and characterisation of a novel P-glycoprotein homologue
 from barley
 JOURNAL Gene 199 (1-2), 195-202 (1997)
 MEDLINE 98019088

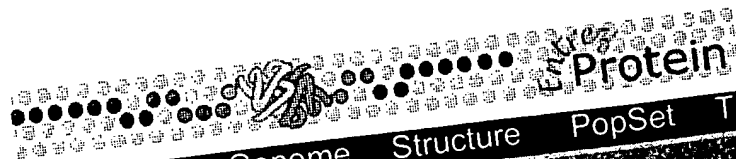
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 241 aekgiiqryt aildktinlg ikqgiakgla vgftglsfai waflawygsr lvmyhhesgg
 301 riyaagisfv lgglslgmal pelkhfieas vaatrileri nrvpqinddd pkglvldqvr
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 541 qhaldqasmg rttlvvahkl stvknadqia vvdggriaei gthdelinkg gpyrslvklq
 601 kmvsyidqet dqfrassaar tsasrlmsmr aspmpltpgf sketesysvp papsfrrlla
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PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

Search Protein ☒ for Limits Index History Clipboard

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☐ 1: T04251 P-glycoprotein 2 - Arabidopsis thaliana BLink, Related Sequences, Taxonomy

LOCUS T04251 1233 aa
 DEFINITION P-glycoprotein 2 - Arabidopsis thaliana.
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 PID g7442648
 VERSION T04251 GI:7442648
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 genetic: #gene pgp2 #map_position 4 #introns 81/3; 100/1; 158/3;
 225/3; 312/2; 492/3; 619/2; 752/1; 832/ 3; 915/2; 1053/1; 1166/3
 #note F20B18.70;
 superfamily: multidrug resistance protein; ATP-binding cassette
 homology;
 PIR dates: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change
 21-Jan-2000.

KEYWORDS
 SOURCE ORGANISM
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 Arabidopsis thaliana

REFERENCE
 AUTHORS
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 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsis.

TITLE
 JOURNAL
 1 (residues 1 to 1233)
 Bevan, M., Rose, M., Hempel, S., Entian, K.D., Hoheisel, J., Mewes, H.W.,
 Mayer, K.F.X. and Schueller, C.

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 Direct Submission
 Submitted (??-MAR-1999) to the Protein Sequence Database

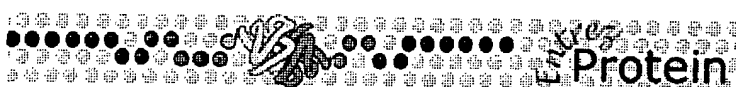
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 /note="ATP-binding cassette homology #label ABC"

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 181 wqislvtsli vplialaggi yafvaiglia rvrksyikag eiaeevignv rtvqftgee
 241 ravrllyreal entykygrka gltkglglgs mhcvlflswa llvwftsvvv hkdiadggks
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 361 iqfkdatfsy psrpdvvifd rlnlaipagk ivalvggsgs gkstvislie rfyepisgav
 421 lldgnnisel dikwlrqqig lvnqepalfa ttirenilyg kddataeeit raaklseais
 481 finnlpegfe tqvgergiql sggqkqriai sraivknpsi llldeatsal daeseksvqe
 541 aldrvmvgtr tvvvahrilst vrnadiiavv hegkivefgn henlisnpgd ayssllrlqe
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 661 smirpdmwyg vcgticafia gsqmplfalg vsqalvsyys gwdetqkeik kiailfccas
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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search	Protein	for				Go	Clear
Limits		Index		History		Clipboard	
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: T05802 **hypothetical protein M7J2.180 -**
Arabidopsis thaliana

BLink, Related Sequences, Taxonomy

LOCUS T05802 280 aa PLN 17-MAR-2000
DEFINITION hypothetical protein M7J2.180 - Arabidopsis thaliana.
ACCESSION T05802
PID g7486813
VERSION T05802 GI:7486813
DBSOURCE pir: locus T05802;
summary: #length 280 #molecular-weight 30185 #checksum 9046;
genetic: #map_position 4 #introns 89/3; 119/3; 164/3; 183/3; 202/3
#note M7J2.180;
superfamily: inner membrane protein malK; ATP-binding cassette
homology;
PIR dates: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change
17-Mar-2000.

KEYWORDS .
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (residues 1 to 280)
AUTHORS Bevan, M., Barges, M., Perez-Perez, A., Terol, J., Torres, A.,
Perez-Alonso, M., Hoheisel, J., Mewes, H.W., Mayer, K.F.X. and
Schueller, C.
TITLE Direct Submission
JOURNAL Submitted (??-APR-1998) to the Protein Sequence Database

FEATURES Location/Qualifiers
source 1..280
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
Protein 1..280
/product="hypothetical protein M7J2.180"

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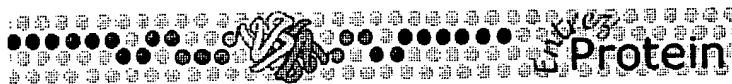
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Restrictions on Use | Write to the HelpDesk
NCBI | NLM | NIH

PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
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☐ 1: [AAC13635](#) **F6N23.3 gene product** BLink, Related Sequences, Nucleotide, Taxonomy
[Arabidopsis thaliana]

LOCUS AAC13635 213 aa PLN 12-NOV-1999
 DEFINITION F6N23.3 gene product [Arabidopsis thaliana].
 ACCESSION AAC13635
 PID g3047124
 VERSION AAC13635.1 GI:3047124
 DBSOURCE locus F6N23 accession [AF058919.2](#)
 KEYWORDS .
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 ORGANISM *Arabidopsis thaliana*
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 213)
 AUTHORS Geisel,C.
 TITLE The sequence of A. thaliana F6N23
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 213)
 AUTHORS Washington University Genome Sequencing Center.
 TITLE The A. thaliana Genome Sequencing Project
 JOURNAL Unpublished
 REFERENCE 3 (residues 1 to 213)
 AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (10-APR-1998) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 REFERENCE 4 (residues 1 to 213)
 AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (12-NOV-1999) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT Method: conceptual translation.
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 121 nrstkqnksp prcvafasd lifatislnp hrregmsvaa lsldhsmwfh rpvraddwll
 181 fvivsptate srgfatgkmf nrkgevrcci eee



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search: Protein		[X] for		[Go]		[Clear]	
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Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: AAF17668 **F20B24.12** [Arabidopsis thaliana] BLINK, Related Sequences, Nucleotide, Taxonomy

LOCUS C009398 17 1316 aa PLN 11-OCT-2000
 DEFINITION F20B24.12 [Arabidopsis thaliana].
 ACCESSION AAF17668
 PID g6573748
 VERSION AAF17668.1 GI:6573748
 DBSOURCE locus AC009398 accession AC009398.6
 KEYWORDS .
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Eudicotyledons; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 1316)
 AUTHORS Shinn,P., Brooks,S., Buehler,E., Chao,Q., Johnson-Hopson,C., Khan,S., Kim,C., Altafi,H., Bei,Q., Chin,C., Chiou,J., Choi,E., Conn,L., Conway,A., Gonzales,A., Hansen,N., Howing,B., Koo,T., Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharsky,N., Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J., Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Federspiel,N.A., Theologis,A. and Ecker,J.R.
 TITLE Genomic sequence for Arabidopsis thaliana BAC F20B24 from chromosome I
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 1316)
 AUTHORS Ecker,J.R.
 TITLE Direct Submission
 JOURNAL Submitted (21-AUG-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
 REFERENCE 3 (residues 1 to 1316)
 AUTHORS Ecker,J.R.
 TITLE Direct Submission
 JOURNAL Submitted (06-NOV-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
 REFERENCE 4 (residues 1 to 1316)
 AUTHORS Chao,Q., Brooks,S., Buehler,E., Johnson-Hopson,C., Khan,S., Kim,C., Shinn,P., Altafi,H., Bei,B., Chin,C., Chiou,J., Choi,E., Conn,L., Conway,A., Gonzalez,A., Hansen,N., Howing,B., Koo,T., Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,J., Liu,S., Mukharsky,N., Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J., Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Davis,R., Federspiel,N., Theologis,A. and Ecker,J.
 TITLE Direct Submission
 JOURNAL Submitted (14-DEC-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA
 REFERENCE 5 (residues 1 to 1316)
 AUTHORS Chao,Q., Brooks,S., Buehler,E., Johnson-Hopson,C., Khan,S., Kim,C., Shinn,P., Altafi,H., Bei,B., Chin,C., Chiou,J., Choi,E., Conn,L., Conway,A., Gonzalez,A., Hansen,N., Howing,B., Koo,T., Lam,B.,

Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N.,
 Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A.,
 Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R.,
 Federspiel, N., Theologis, A. and Ecker, J.

TITLE Direct Submission

JOURNAL Submitted (11-OCT-2000) Arabidopsis thaliana Genome Center,
 Department of Biology, University of Pennsylvania, 38th and
 Hamilton Walk, Philadelphia, PA 19104-6018, USA

COMMENT Method: conceptual translation.

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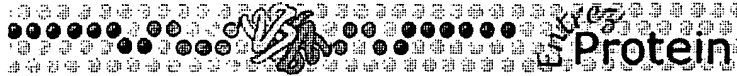
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421 fvipagkvva lvvgsgsgks tmislierfy eptdgavmld gndiryldlk wlrghiglvn
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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search		Protein	for				Go Clear
Limits		Index		History		Clipboard	
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: [BAA96612](#) **Similar to Arabidopsis thaliana chromosome 2, BAC F14M4 ; putative ABC transporter (AC004411) [Oryza sativa]** BLink, Related Sequences, Nucleotide, Taxonomy

LOCUS BAA96612 1285 aa PLN 10-JUN-2000
 DEFINITION Similar to Arabidopsis thaliana chromosome 2, BAC F14M4 ; putative ABC transporter (AC004411) [Oryza sativa].

ACCESSION BAA96612
 PID g8468012
 VERSION BAA96612.1 GI:8468012
 DBSOURCE locus AP002482 accession [AP002482.1](#)
 KEYWORDS .
 SOURCE Oryza sativa.

ORGANISM *Oryza sativa*

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

REFERENCE 1 (residues 1 to 1285)
 AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
 TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0706B05

JOURNAL Published Only in DataBase (2000) In press
 REFERENCE 2 (residues 1 to 1285)
 AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
 TITLE Direct Submission
 JOURNAL Submitted (07-JUN-2000) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail:tsasaki@abr.affrc.go.jp,
 URL:http://www.dna.affrc.go.jp:82/, Tel:81-298-38-7441,
 Fax:81-298-38-7468)

COMMENT The orientation of the sequence is from T7 to SP6 of the PAC clone. Genes were predicted from the integrated results of the following:GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against the non-redundant database NRP (PIR, SWISSPROT, GENPEPT, PDB) from MAFF DNA bank and the cDNA sequence database at RGP. Protein similarities of the coding regions were searched against NRP with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN2.0 with the corresponding DDBJ accession no. and RGP clone ID.
 Detailed information on overlap and assembly quality together with annotation of this entry at
<http://www.dna.affrc.go.jp:82/genomicdata/GenomeFinished.html>.

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241 maslgqaaya essvvveqti gsirtvasft gekqavekyn kslksayksg vreglaaglg
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PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

Search Protein for [] Go Clear

Limits Index History Clipboard

Display Default View as HTML Save Add to Clipboard

1: CAA75922 P-glycoprotein-like protein BLink, Related Sequences, Nucleotide, Taxonomy [Arabidopsis thaliana]

LOCUS CAA75922 1229 aa PLN 28-DEC-1997
 DEFINITION P-glycoprotein-like protein [Arabidopsis thaliana].
 ACCESSION CAA75922
 PID g2739309
 VERSION CAA75922.1 GI:2739309
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 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
 Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 1229)
 AUTHORS Sidler, M. and Dudler, R.
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 1229)
 AUTHORS Dudler, R.
 TITLE Direct Submission
 JOURNAL Submitted (19-DEC-1997) R. Dudler, University of Zurich, Institute
 of Plant Biology, Zollikerstrasse 107, CH-8008 Zurich, Switzerland
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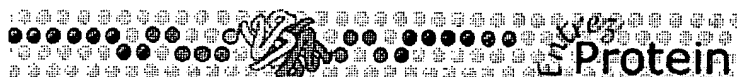
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NCBI | NLM | NIH



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search		Protein	for				Go
Limits		Index		History		Clipboard	
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: [AAF76889](#) **ABC transporter** BLINK, Related Sequences, Nucleotide, Taxonomy, LinkOut
[Mus musculus]

LOCUS AF266284_1 715 aa ROD 18-JUN-2000
 DEFINITION ABC transporter [Mus musculus].
 ACCESSION AAF76889
 PID g8571454
 VERSION AAF76889.1 GI:8571454
 DBSOURCE locus AF266284 accession [AF266284.1](#)
 KEYWORDS .
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (residues 1 to 715)
 AUTHORS Shirihi, O.S., Gregory, T., Yu, C., Orkin, S.H. and Weiss, M.J.
 TITLE ABC-me: A Novel Mitochondrial Transporter Induced by GATA-1 During
 Erythroid Differentiation
 JOURNAL EMBO J. (2000) In press
 REFERENCE 2 (residues 1 to 715)
 AUTHORS Shirihi, O., Orkin, S.H., Gregory, T. and Weiss, M.J.
 TITLE Direct Submission
 JOURNAL Submitted (10-MAY-2000) Hematology-316 ARC, Children's Hospital of
 Philadelphia, 34th and Civic Center Blvd, Philadelphia, PA 19104,
 USA
 COMMENT Method: conceptual translation supplied by author.
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ORIGIN

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Search Protein		for		Go		Clear	
Limits		Index		History		Clipboard	
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: AAC34225 putative ABC transporter [Arabidopsis thaliana] BLink, PubMed, Related Sequences, Nucleotide, Genome, Taxo

LOCUS AAC34225 1286 aa PLN 05-APR-2000
 DEFINITION putative ABC transporter [Arabidopsis thaliana].
 ACCESSION AAC34225
 PID g3522943
 VERSION AAC34225.1 GI:3522943
 DBSOURCE locus AC004411 accession AC004411.2
 KEYWORDS .
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 1286)
 AUTHORS Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D.,
 Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E.,
 Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M.,
 Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L.,
 Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H.,
 Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D.,
 Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
 Venter,J.C.
 TITLE Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana
 JOURNAL Nature 402 (6763), 761-768 (1999)
 MEDLINE 20083487
 PUBMED 10617197
 REFERENCE 2 (residues 1 to 1286)
 AUTHORS Lin,X.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 COMMENT Method: conceptual translation.
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901 sqvandavgs irtvasfcae dkvmnmyskk cegpmkngir qgivsgigfg fsffvlfssy
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Restrictions on Use | Write to the HelpDesk
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PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM
 Search Protein ☒ for Limits Index History Clipboard
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☐ 1: CAB83120 ABC transporter-like
 protein [Arabidopsis
 thaliana]

BLink, Related Sequences, Nucleotide, Taxonomy

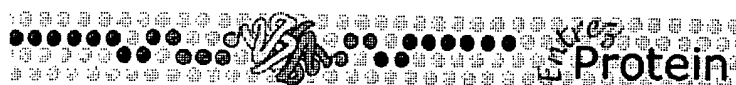
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 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
 Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 1539)
 AUTHORS Bloecker, H., Mewes, H.W., Rudd, S., Lemcke, K., Mayer, K.F.X.,
 Quetier, F. and Salanoubat, M.
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 1539)
 AUTHORS EU Arabidopsis sequencing, project.
 TITLE Direct Submission
 JOURNAL Submitted (29-MAR-2000) MIPS, at the Max-Planck-Institut fuer
 Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
 lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project
 Coordinator: Marcel Salanoubat and Francis Quetier, Groupement
 d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue
 Gaston Cremieux, BP191, 91006 Evry Cedex, France;
 http://www.genoscope.cns.fr
 COMMENT Information on performance of analysis and a more detailed
 annotation of this entry and other sequences of chromosomes 3, 4
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 AA674-681;ATP/GTP-binding site motif A (P-loop)
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ORIGIN

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241 veksenvsly asasfisktf wlwmnp1lrk gyksplndq vptlspehra eklatlfsk
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☐ 1: CAA72120 **multi resistance protein** BLink, Related Sequences, Nucleotide, Taxonomy
[Arabidopsis thaliana]

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 DEFINITION multi resistance protein [Arabidopsis thaliana].
 ACCESSION CAA72120
 PID g2980641
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 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 Rosidae; Capparales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 1514)
 AUTHORS Weigmann,N., Ansorge,M. and Mueller-Roeber,B.
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 1514)
 AUTHORS Weigmann,N.
 TITLE Direct Submission
 JOURNAL Submitted (14-FEB-1997) N. Weigmann, MPI of Molecular Plant
 Physiology, Mueller-Roeber, Karl-Liebknechtstr.25, Haus 20, 14476
 Golm, FRG

FEATURES Location/Qualifiers
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ORIGIN

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Restrictions on Use | Write to the HelpDesk
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1: T00961 hypothetical protein F20D22.11 - Arabidopsis thaliana

[BLink, Related Sequences, Taxonomy](#)

LOCUS T00961 1355 aa PLN 04-MAR-2000
 DEFINITION hypothetical protein F20D22.11 - Arabidopsis thaliana.
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 VERSION T00961 GI:7485868
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 cassette homology;
 PIR dates: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
 04-Mar-2000.

KEYWORDS .
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (residues 1 to 1355)
 AUTHORS Vysotskaia,V.S., Osborne,B.I., Schwartz,J.R., Toriumi,M., Kwan,A.,
 Yu,G., Oji,O., Liu,S., Li,J., Hoang,L., Araujo,R., Au,M.,
 Brendel,V., Buehler,E., Conway,A.B., Conway,A.R., Dewar,K.,
 Feng,J., Kim,C., Kurtz,D., Li,Y., Palm,C.J., Shinn,P., Sun,H.,
 Davis,R.W., Ecker,J.R., Federspiel,N.A. and Theologis,A.

TITLE Direct Submission
 JOURNAL Submitted (??-MAY-1998) to the EMBL Data Library

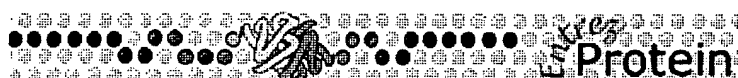
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☐ 1: [AAD25615](#) Similar to

BLink, Related Sequences, Nucleotide, Taxonomy

**ABC-transporter
atp-binding protein
[Arabidopsis thaliana]**

LOCUS C005287_17 514 aa PLN 10-DEC-1999
 DEFINITION Similar to ABC-transporter atp-binding protein [Arabidopsis thaliana].
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 VERSION AAD25615.1 GI:4585979
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 KEYWORDS .
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 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (residues 1 to 514)
 AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vysotskaia,V.S., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 514)
 AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Kurtz,D.B., Conway,A.R., Au,M., Araujo,R., Buehler,E., Dewar,K., Feng,J., Kim,C., Li,Y., Oji,O., Osborne,B.I., Shinn,P., Sun,H., Toriumi,M., Vyotskaia,V., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
 TITLE Direct Submission
 JOURNAL Submitted (15-JUL-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

REFERENCE 3 (residues 1 to 514)
 AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

REFERENCE 4 (residues 1 to 514)
 AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
 TITLE Direct Submission
 JOURNAL Submitted (17-APR-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

REFERENCE 5 (residues 1 to 514)
AUTHORS Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Brooks, S., Buehler, E., Chao, Q., Dunn, P., Gonzalez, A., Khan, S., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT Method: conceptual translation supplied by author.
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 Protein 1..514
 /name="Similar to ABC-transporter atp-binding protein"
 CDS 1..514
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ORIGIN
 1 mtkyyllqryl kdqtfykiqs qsiidnpdqr lvddlssftg talsfsltlv natidlisfs
 61 nilftiyppl flvlllysfg gtaisvflgk glvnlfnlqe kkeadfrysl vrvrenaesi
 121 afyggeqnem qlllqrfrsa fdnltellia srnlefftdg yryliqilpv avvapmyfsg
 181 kiefgvinqs vsafnhilgd fslvvyqfqa issfsavidr lgefddlldn nifrdpsdtv
 241 deieltyqse mnsslldtng siksqpnqkr leieeltlqt ptngttlvhv lsadvydkdh
 301 llimgpsgsg ktsllramag lwrsgkgkit ekrrrivpst kalygsgifa saialsylec
 361 ncsppllire dgnekpttd lmrlekvcl ghiadrfggl dsihewssvl slgeqqrlaf
 421 arlllsqpk lalldestsal deaneaflyq qiqsagityi sighrrtltk fhnilqist
 481 adpksnernw riedvdaqds lygrlnqkev pses
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PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

Search Protein for Limits Index History Clipboard

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BLink, Related Sequences, Taxonomy

1: T06091 hypothetical protein T5J17.20 - Arabidopsis thaliana

LOCUS T06091 1383 aa
DEFINITION hypothetical protein T5J17.20 - Arabidopsis thaliana.
ACCESSION T06091
PID g7487703
VERSION T06091 GI:7487703
DBSOURCE pir: locus T06091;
summary: #length 1383 #molecular-weight 154829 #checksum 8482;
genetic: #gene ATSP:T5J17.20 #map_position 4 #introns 21/2; 116/3;
191/3; 257/3; 409/2; 454/3; 481/1; 558/3; 660/ 2; 704/3; 756/3;
831/1; 867/2; 897/3; 953/3; 992/2; 1070/3; 1131/1; 1198/1; 1247/1;
1325/1;
PIR dates: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change
22-Oct-1999.

KEYWORDS thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (residues 1 to 1383)
AUTHORS Bevan, M., Murphy, G., Ridley, P., Hudson, S., Bancroft, I., Mewes, H.W.,
Mayer, K.F.X. and Schueller, C.
TITLE Direct Submission
JOURNAL Submitted (??-MAR-1999) to the Protein Sequence Database

FEATURES
source Location/Qualifiers
1..1383
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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ORIGIN
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121 alsnlrakvq gflfraaflr raplflrlis enimlcfmls tlhstskyit galslrfrki
181 ltkiihshyf enmvvykshv vdgrithpeq riasdvprfs selsdlildt ltavtdgily
241 awrlcsyasp kyifwilayv lgagtairnf spsfgklmsk eqqlegeyrq lhrslrthse
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361 fsghlrpdds tlgraemlsn iryhtsviis lfqalgtlsi ssrrlnrlsg yadrihelma
421 vsrelsgddk ssfqnrnsrn ylseanyvef sdvkvtptg nvlvedltlr veqgsnllit
481 gglwplvsgh ivkpgvgsdl nkeifyvpqr pymavgtlrd qliypitgsg esellteigm
541 vellknvsil vslfytrmvd leylddryqp ekevnwgdsl slgeqqrldg arlfyhhpkpf
601 aildectsav ttdmeerfaa kvramgtsci tishrpalva fhdvvlslldg eggwsvhykr
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721 arspvvdksv vlprfpqpt sqralpsrva amlnvlpwk phllfcistw ltysscadan
781 idiillkitd hfivtfqipt ifdkqgaqll avaclvsrt lisdrialsn gttvkylvleq
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1261 rdiwptvcgr ltkpsldike lgsgngmffv pqrpytclgt lrdqiypis keeaekraak
1321 lytsgeeste agsildshlk tilenvrlvy llerdvggwd attnwedils lgeqqrlgmv
1381 sll

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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search	Protein	for				Go	Clear
Limits	Index	History	Clipboard				
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: AAD03441 contains similarity to **Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]** BLink, Related Sequences, Nucleotide, Taxonomy

LOCUS AAD03441 557 aa PLN 10-AUG-1999
DEFINITION contains similarity to Guillardia theta ABC transporter
(GB:AF041468) [Arabidopsis thaliana].
ACCESSION AAD03441
PID g4115931
VERSION AAD03441.1 GI:4115931
DBSOURCE locus T4B21 accession AF118223.2
KEYWORDS .
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (residues 1 to 557)
AUTHORS Abbott,A., Kock,J. and Lehnert,L.
TITLE The sequence of A. thaliana T4B21
JOURNAL Unpublished
REFERENCE 2 (residues 1 to 557)
AUTHORS Washington University Genome Sequencing Center.
TITLE The A. thaliana Genome Sequencing Project
JOURNAL Unpublished
REFERENCE 3 (residues 1 to 557)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (06-JAN-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 4 (residues 1 to 557)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (06-AUG-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 5 (residues 1 to 557)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT Method: conceptual translation.
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CDS

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ORIGIN

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301 ivaeegsfve ylegctapsy dtnqlhaavv elyqgkga ei kystvqnwya gdegkkggiy
361 nfvtkrglca gdrskiswtq vetgsaitwk ypsvvlegdd svgefysval tnnyqqadtg
421 tkmihkgknt ksriiskgis aghsrncyrq lvqvqskaeg akntstcdsm ligdkaaant
481 ypyiqvknp akveheasts kigedqlfyf qrgidhera laamisgfc dvfnklpdef
541 gaevnqlmsi klegsvg
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Search		Protein	for					Go	Clear
Limits		Index		History		Clipboard			
Display	Default View	as	HTML	Save	Add to Clipboard				

☐ 1: AAD04949 putative ethylene response BLink, Related Sequences, Nucleotide, Taxonomy sensor [Phalaenopsis sp. 'KCbutterfly']

LOCUS AAD04949 633 aa PLN 14-JAN-1999
 DEFINITION putative ethylene response sensor [Phalaenopsis sp. 'KCbutterfly'].
 ACCESSION AAD04949
 PID g4154359
 VERSION AAD04949.1 GI:4154359
 DBSOURCE locus AF113541 accession AF113541.1
 KEYWORDS .
 SOURCE Phalaenopsis sp. 'KCbutterfly'.
 ORGANISM Phalaenopsis sp. 'KCbutterfly'
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Phalaenopsis.
 REFERENCE 1 (residues 1 to 633)
 AUTHORS Chai, I.J., Lee, B.H., Wang, W.K., Liang, C.C. and Lin, C.Y.
 TITLE Molecular cloning of the Phalaenopsis sp. 'KCbutterfly' ethylene response sensor cDNA
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 633)
 AUTHORS Chai, I.J., Lee, B.H., Wang, W.K., Liang, C.C. and Lin, C.Y.
 TITLE Direct Submission
 JOURNAL Submitted (14-DEC-1998) King Car Food Industrial Co. LTD., Yuan-Shan Research Institute, 86 Chin-Hsiang Road, Yuan Shan, I-Lan 264, Taiwan, R.O.C.
 COMMENT Method: conceptual translation supplied by author.
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 source Location/Qualifiers
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 /db_xref="taxon:86001"
 /tissue_type="petal"
 Protein 1..633
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 CDS 1..633
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ORIGIN

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181 lwmpsrtgln lqlshtlnnq ipvgsvvsin lpvvnqvfnv sravriphtc qlarfqphtg
241 ryvppevvav rvpllhlsnf qindwpelsa knfavmvlml psdsarkwhv yelevelvevva
301 dqvavalsha aileesmrar dqlmdqnvat dlarreaema irarndflav mnhemrtpmh
361 aiaalsslll eteltpeqrl mvetilkssn llatlindvl dlskledgsf elevtvfnlh
421 tvfrevvnli kpiaavkklv livslspdlp scavgdekrl mqtmlnvvgv avkftkegsi
481 sitasiakpd slrdprdpf ypipsgghfy lrvqikdtgc gispqelphl ftkfahaqng
541 sdkgyngsgl glaickrfvn lmkghiwles egigkgctti fivklgised pahryqhkll
601 ppiragqsea dafgskrmpt dliplknryq rsl

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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search	Protein	for		Go	Clear		
Limits	Index	History	Clipboard				
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: BAA85819 **ethylene receptor** BLink, PubMed, Related Sequences, Nucleotide, Taxonomy
CS-ETR2
[Cucumis
sativus]

LOCUS BAA85819 767 aa PLN 30-MAY-2000
 DEFINITION ethylene receptor CS-ETR2 [Cucumis sativus].
 ACCESSION BAA85819
 PID g6136818
 VERSION BAA85819.1 GI:6136818
 DBSOURCE locus AB026500 accession AB026500.1
 KEYWORDS .
 SOURCE cucumber.
 ORGANISM Cucumis sativus
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Cucurbitales;
 Cucurbitaceae; Cucumis.
 REFERENCE 1 (sites)
 AUTHORS Yamasaki,S., Fujii,N. and Takahashi,H.
 TITLE The ethylene-regulated expression of CS-ETR2 and CS-ERS genes in
 cucumber plants and their possible involvement with sex expression
 in flowers
 JOURNAL Plant Cell Physiol. 41 (5), 608-616 (2000)
 MEDLINE 20383769
 REFERENCE 2 (residues 1 to 767)
 AUTHORS Yamasaki,S., Fujii,N. and Takahashi,H.
 TITLE Direct Submission
 JOURNAL Submitted (21-APR-1999) Seiji Yamasaki, Institute of Genetic
 Ecology, Tohoku University; Katahira 2-1-1 Aoba-ku, Sendai, Miyagi
 980-8577, Japan (E-mail:yamasaki@bansui.ige.tohoku.ac.jp,
 Tel:81-22-217-5715(ex.5715), Fax:81-22-263-9845)
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 Protein 1..767
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 CDS 1..767
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 /coded_by="AB026500.1:330..2633"
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 121 vscataitli tliplllkvk vrefmlkekt wdlgrevgmi lkqkeaglhv rmltqeirks
 181 ldrhtilytt mfelsetlgl hycavwmpne sktlmnlthe lkdrsfsgny nvfipisdsd
 241 vikikgsdgv nvlgpnsalv vancgesder gpaaairmpm lrvsnfkgtt peivptyyai
 301 lvlvlpggqp rswnngelei ikvvadqvav alshaallee sqldmrklae qnrdlqqake
 361 nalmasqarn sfqkvmsdgm rrpmsimlgl lsmlqnenmn ddqriildam vrtgnvvstq
 421 iddvmehpik dsarfplele mrsfrlhsmi keaaclakcl caykgfgfaf evqrslpdhv
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 541 irfevginks nsqsegsipn mvsgdrryas dgaeerlsft ickklvklmq gniwvipnpq
 601 gftrsmalvl rfqlrpslav ampepgesse hphsnsifrg lqviladadd mnrvatrkm
 661 eklgcnvtav ssgfecltvm apagssiqvv lldlhmpeld gfevttrirk frsqnyrpvi
 721 ialtasaged wercvqigmn gvirkpvqlq giahelrral lqaskvv



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	
Search	Protein	for					Go	Clear
Limits		Index	History	Clipboard				
Display	Default View	as	HTML	Save	Add to Clipboard			

☐ 1: P47924 **GTP CYCLOHYDROLASE II** BLink, PubMed, Related Sequences, Taxonomy

LOCUS GCH2_ARATH 245 aa PLN 30-MAY-2000
 DEFINITION GTP CYCLOHYDROLASE II.
 ACCESSION P47924
 PID g1346113
 VERSION P47924 GI:1346113
 DBSOURCE swissprot: locus GCH2_ARATH, accession P47924;
 class: standard.
 created: Feb 1, 1996.
 sequence updated: Feb 1, 1996.
 annotation updated: May 30, 2000.
 xrefs: gi: gi: 940382, gi: gi: 940383
 xrefs (non-sequence databases): PFAM PF00925
 KEYWORDS Riboflavin biosynthesis; Hydrolase.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
 Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 245)
 AUTHORS Kobayashi, M., Sugiyama, M. and Yamamoto, K.
 TITLE Isolation of cDNAs encoding GTP cyclohydrolase II from Arabidopsis
 thaliana
 JOURNAL Gene 160 (2), 303-304 (1995)
 MEDLINE 95369709
 REMARK SEQUENCE FROM N.A.
 COMMENT

 This SWISS-PROT entry is copyright. It is produced through a
 collaboration between the Swiss Institute of Bioinformatics and
 the EMBL outstation - the European Bioinformatics Institute.
 The original entry is available from <http://www.expasy.ch/sprot>
 and <http://www.ebi.ac.uk/sprot>

[CATALYTIC ACTIVITY] GTP + 3 H(2)O = FORMATE +
 2,5-DIAMINO-6-HYDROXY-4-(5-PHOSPHORIBOSYLAMINO)PYRIMIDINE +
 PYROPHOSPHATE.

[PATHWAY] RIBOFLAVIN BIOSYNTHESIS.

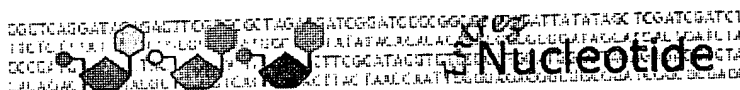
[SIMILARITY] BELONGS TO THE GTP CYCLOHYDROLASE II FAMILY.

FEATURES Location/Qualifiers
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 Protein 1..245
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 181 mttnnpakyvg lkgyglaivg rvpllsitk enkryletkr tkmgmhyglk fkgdvvekie
 241 seses

//



☐ 1: [U92650](#) *Arabidopsis thaliana* MRP-like PubMed, Protein, Related Sequences, Taxonomy
ABC transporter mRNA,
complete cds

01/30/2001 8:34 AM

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 FRFRSDNMRLSDVTLGPNSIQLGAMEWLCFRDLMLSSLTFCLFNWFSWSPIPTGVIDP
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 SWPSRGEVEIRDLQVRYAPHMPLVLRGITCTFKGGLRTGIVGRTGSGKSTLIQTLFRI
 VEPSAGEIRIDGVNILTIGLHDLRLRLSIIIPQDPTMFEGTMRSLNDPLEEYTDQIWE
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 VDTATDNLIQKTLREHFSDCTVITIAHRISSVIDSDMVLLLSNGIIIEEYDTPVRILLED
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BASE COUNT 1256 a 901 c 1155 g 1497 t
 ORIGIN

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2221 taagggtgctt gaagcatgtt cgttgagtaa ggaatctggag atactttcat tcggtgatca
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